

Db 251 CACCAAGACCTGCAGGATCTGTCTATCTTTCATCACCAATGTCCATACCAACTCGGG 310
Qy 723 CCTTACACCTGCAATGTGTCGGGAGTTTGAGTTTGAGGCGGATCGGCCCTTTGTGAA 782
Db 311 CGACTACAGTGCACCGTCTACCGCTGCTCTTCTTCGAAAACTACGAGCAACACCG 370
Qy 783 GACGACGGGTGATCCCTTAAGAGTCAACGAGGCTGAGGAGGACTTCACCTCTGT 842
Db 371 CGTGTCAAGAGATCCATTTAGGTAGTGCACAAAGCCAAAGACATGGCATCAT 430
Qy 843 GGTCTCAGAAATCATGATGATCATCTTCTGTTCTTCTTCCATCCCTGTGGTGTCTCATGA 902
Db 431 CGTGTCTCAGATCATGATGATGCTCATTTGTGTTGACCATATGGCTCGTGGCAGA 490
Qy 903 GATGATATATTGCTACAGAAAGTCTCAAAAGCCGAAGAG---CGAGCCCAAGAAAGCG 959
Db 491 GATGATTTACTGCTACAGAAAGATCGCTGCGCCCAACGAGACTGCTGCACAGGAGATGC 550
Qy 960 GTCTGACTACCTTGCCATCCCATCTTGAGAACCAAGAGAACTCTCGGG 1006
Db 551 CTCGAATACCTGGCCATCACCTCTGAAAGCAAGAGAACTGCACGG 597

RESULT 2

US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111

Query Match 4.0%; Score 51; DB 3; Length 11174;
Best Local Similarity 58.1%; Pred. No. 0.0045;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 441 CTTCCCTGTGTGTGTGGAAGTCCCTCGAGACGAGGCGGTGACAGGCAACCCCATGAA 500
Db 2011 CTCGGGGGCTGCGTGGAGGTGGAAGTCCGAGACCGAGGCGGTGTATGGATGACCTTCAA 2070
Qy 501 GCTGCGCTGCATCTCTCATGAAGAGAGAGGTGGAGGCCACACGCTGGTGAATG 560
Db 2071 AATTTTTCATCTCTCTGAAGCGCCGAGCGAGACCAACGCTGAGACCTTCAACGAGTG 2130
Qy 561 GTTCTACAGGCCGCGGCGGTAAAGATTTCCTTA 595
Db 2131 GACCTTCGCCAGAGGGCACTGAGAGTTTGTCA 2165

RESULT 3

US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13053
; LENGTH: 30337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(30337)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053

Query Match 3.9%; Score 48.6; DB 3; Length 30337;
Best Local Similarity 63.0%; Pred. No. 0.028;
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 829 GACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGTGTTCTTCTCACCTG 888
Db 620 GACATGCGATCCATCGTGTCTGAGATCATGATGATGCTCATTTGTTGTTGACCAT 679
Qy 889 TGGTGTCTCATCGAGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAAGGCGACG 947
Db 680 TGGCTCGTGGCAGAGATGATTTACTGCTACAAGAGATCGTGCAGGACGAGACTGC 738

RESULT 4

US-09-023-587A-5
; Sequence 5, Application US/09023587A
; Patent No. 6653530
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, Christine K.
; APPLICANT: Bhat, Ganesh B.
; APPLICANT: Venkatramesh, Mylavaram
; APPLICANT: Rangwala, Shaikat H.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Boddupalli, Sekhar S.
; TITLE OF INVENTION: Methods for Producing Carotenoid Compounds, Tocopherol Compounds,
; Specialty Oils in Plant Seeds
; FILE REFERENCE: 16516.122
; CURRENT APPLICATION NUMBER: US/09/023,587A
; CURRENT FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Zea mays
US-09-023-587A-5

Query Match 3.6%; Score 45.4; DB 3; Length 1645;
Best Local Similarity 46.2%; Pred. No. 0.068;
Matches 151; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
Qy 429 GGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGGAGGCCGTGCAGGG 488
Db 349 GGTGTCACGGCTCTTCTTAAGGTACGAGGCCGCCCAAGAGCGGTCTGTACGT 408
Qy 489 CAACCCCATGAAGCTGCGCTGCATCTCTGTCATGAAGAGAGAGGATGAGGCCACCCAC 548
Db 409 GGTGCACTACAAACCACTACGACGCGCAGCAACGCGCAAGTTCGCGCGCGAGAACGCTCGTT 468

Db 4948 GACTTCTCCAGGACCTGGTGGACCTGGCTCGAAGATGACGGACGGCGGCACCTC 4889
Qy 496 ATGAGCTGCGCTGCATCTCTGCATGAAGAGAGAGAGGAGGAGGACACCGTGGTG 555
Db 4888 ATCCACCGCGCTGGTGGCGTCTTCGCGACGGGTGACAGCATCGTCGGCAACAACCTGGTG 4829
Qy 556 GAATGGTTCTACAGCGCCGAGGGCGGTAAAGATTTCCTTTATTACGAGTATCGGAATGGC 615
Db 4828 CTGAACCTCTACAGCACTGAAGCCCTGAGGGCGGAGTACCTGTCCGCGCAGCTC 4769
Qy 616 CACGAGGAGTG 627
Db 4768 TACGAGGAGCG 4757

RESULT 8
US-09-902-540-4106/c
; Sequence 4106, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4106
; LENGTH: 2133
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4106

Query Match 3.4%; Score 42.4; DB 3; Length 2133;
Best Local Similarity 51.6%; Pred. No. 0.46; Mismatches 91; Indels 0; Gaps 0;
Matches 97; Conservative 0;
Qy 462 GCCCTCGGAGAGCGGAGCGCGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTCGCAT 521
Db 1813 GCCCAGGATGATGGCGGGCGCCATCCGCTTGAAGACGCGTGCAAGCGCGCGTGCAG 1754
Qy 522 GAAGAGAGAGAGTGGAGGCCACACCGGTGGTGAATGGTTCTACAGGCCCGCGAGGGCGG 581
Db 1753 GAAAGCGGGCGGAGTGGGACACGCTGGGCGTGGGACCGCTTCCACGACCAAGTGTGCT 1694
Qy 582 TAAAGATTCTTATTACGAGTATCGGAATGGCCACGAGGAGTGGAGAGCCCTTTCA 641
Db 1693 GGGTGAAGCGTCCGCTAGAGATCTGCGGGAATCTCCAGCTCGGACAGCGCGCGGTGCA 1634
Qy 642 GGGGCGCC 649
Db 1633 GCTCCGCC 1626

RESULT 9
US-09-902-540-1203
; Sequence 1203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1203
; LENGTH: 23738
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1203
Query Match 3.4%; Score 42.4; DB 3; Length 23738;
Best Local Similarity 51.6%; Pred. No. 1.1; Mismatches 91; Indels 0; Gaps 0;
Matches 97; Conservative 0;
Qy 462 GCCCTCGGAGAGCGGAGCGCGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTCGCAT 521
Db 4191 GGCCAGGATGATGGCGGGCGGCCATCCCGTTTGAAGACGCGTGAAGCGCGCGTGCAG 4250
Qy 522 GAAGAGAGAGAGTGGAGGCCACCGCGTGGTGGATGGTTCTACAGGCCCGAGGGCGG 581
Db 4251 GAAAGCGGGCGGAGTGGGACACGCTGGGCGTGGGACCGCTTCCAGACACCAAGTGTGCT 4310
Qy 582 TAAAGATTCTTATTACGAGTATCGGAATGGCCACGAGGAGTGGAGAGCCCTTTCA 641
Db 4311 GGGTGAAGCGCTCCGCTACGAGGATCTGCGGGAATCTCCAGAGCGCGCGTGA 4370
Qy 642 GGGGCGCC 649
Db 4371 GCTCCGCC 4378

RESULT 10
US-09-949-016-15003/c
; Sequence 15003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15003
; LENGTH: 9622
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15003
Query Match 3.3%; Score 42; DB 3; Length 9622;
Best Local Similarity 49.5%; Pred. No. 0.99; Mismatches 108; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 38 GAGCAGGACGAGCGCGGAGTGGAGCTGGAGTTCGCGGGTGGGCGGAGCGGACTGTC 97
Db 7138 GCGTGAGGCCCTGTGTGAAGGGGTGCTGCTGCGGTAGGGGCTCTGTTCCATGGCCAGA 7079
Qy 98 CGTGTGCTGAGCGCGCGGAGAGCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGG 157
Db 7078 TCTGCTGCTGGTGGGCGCAGCGCGTGTAGGAAGCATCATGCCCTCCATCGGCTGG 7019
Qy 158 GGAGGTCCAGTGGGTGCTTAGGGCCCAAGCCCCACCCCGGCTCCAAAGCTCCGAGG 217
Db 7018 ACAGGACCTCTGGGGGACAGTGAAGCTTACCCCTGGCTGTGTCCAGCGCCCTCCAGC 6959
Qy 218 GCCTCCCCAGCAGCGGTGCTCGGCCCTTCCTTCGGTC 255
Db 6958 TACACCCGAGCAGCCTCCCTTCTGATCTCTTCTGGAC 6921


```

RESULT 11
US-09-489-039A-3591
; Sequence 3591, Application US/09489039A
; Patent NO. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3591
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3591

```

	Query Match	3.3%;	Score 41.6;	DB 3;	Length 696;
	Best Local Similarity	48.3%;	Pred. No. 0.5;		
	Matches 116;	Conservative 0;	Mismatches 124;	Indels 0;	Gaps 0;
Qy	458	AAGTGCCTCGGAGACGAGGCGCTGCAGGGCAACCCATGAAGCTGCGTGCATCTCCCT	517		
Db	92	AGGCGCGGACGTGCGCAGGCGGTGTGGCAGCTGCCAGCGCGCTATCCGACT	151		
Qy	518	GCATGAAGAGAGAGGAGGTGAGGCCACACGCGTGTGGAAATGTTCTACAGGCCCGAGG	577		
Db	152	ACCTGCCGTTCAACGACGTTTGACGGTACCCCGCTGGATCAGGGGAAITGCGCTGTGGTTCC	211		
Qy	578	CGCGTAAAGATTTCCTTATTTACGAGTATCGGAATGGCCACCGAGGTTGAGAGCCCTC	637		
Db	212	CCGGCCGAACTCTTTTACCGGGGAAGATGTCTTGAGCTCAGGGCCA CGGCGCCCGG	271		
Qy	638	TTCAGGGCGCCTCGCATGGAAATGGCAGCAAGGACCTGCAGGACGTGTTCATCATCTGTC	697		
Db	272	TCATTCTCGACCTCTGCTTTAAACGTTATCTTGACCTTCGCGGGCTGCGATCGCCAGGC	331		

```

RESULT 12
US-09-771-161A-58
; Sequence 58, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-58

```

Query Match 3.3%; Score 41; DB 3; Length 1097;
Best Local Similarity 52.0%; Pred. No. 0.84;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 CCTTCCTTCGAGCTGAGCTTACCTCTGGGCGCAACGAGCGAGCGAGGGCGCGAGTGG 60

```

Db      23  CCCCCGCTCGGGCTCTGAGCGCTCGGGGCGGGGGTGGCGCGCGCTCGCGCGGCGG 82
Qy      61  AAGCTGAGATTCCGGGGTGGGGGGAGGCGACTGTCCGTGGTGCTGAGCGCGCGCGAGA 120
Db      83  CCGACGCTCTCTTTCCGGCGCGCGGGCGGCGCATCGCTGGGCGCGCGGCTGGGGCG 142
Qy     121  GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCGCT 177
Db     143  GCGGGCGCGAGTTGCTCCCGGGCCCCGCTGAGGGCCCCGCGCGCGCGCGCT 199

RESULT 13
US-09-771-161A-59
; Sequence 59: Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: -
; LOCATION: (1)..(3382)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-59

```

	Query Match	3.3%	Score 41	DB 3	Length 3382
	Best Local Similarity	52.0%	Pred. No. 1.3		
	Matches 92	Conservative 0	Mismatches 85	Indels 0	Gaps 0
Qy	1	CCCTCCCTTCCGAGCTGAGCTTACCTCTGGCGCAAAAGCAGCGAGGCGAGGCGCGCGAGTGG	60		
Db	23	CCCCCGGCTCGGGCTGTGACGGCTCTCGGGCCGGGGGTGGCGCGCTGCGCGCGCGCG	82		
Qy	61	AAGCTGAGTTCGGGGTGGCGGGGAGGCGCACTGTCCTGTGTCTGAGCGCCGCGCGAGA	120		
Db	83	CCGACGCTCTCTTCGAGCGCGCGCGCGGCATGCGTGGGCGCGCGCGTGTGGGCG	142		
Qy	121	GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTTCAAGTGGGGTGCCT	177		
Db	143	GCGGGCGCGAGTTGCTCTCCGGGGCCCGGGCTCAGGGCCCGCGCGCGCGCGCT	199		

RESULT 14
US-09-302-540-3929
; Sequence 3929, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3929

```
; LENGTH: 2943
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3929

Query Match          3.2%; Score 40.6; DB 3; Length 2943;
Best Local Similarity 48.9%; Pred. No. 1.5;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGGAGACGAGGCGCTGCAGGGCAACCCATGAAGCTGCGTGCATCTCCTGC 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1831 GTGCTGGAAGAGTGGAGCGCGCTGGCCGAGCTGGCGCTGATGCCCGGAGGCCGCG 1890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 520 ATGAAGAGAGAGGAGTGGAGGCCACACACGCTGCTGGAATGTTCTACAGGCCCGAGGGC 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1891 ATGGCTACGCGCAGAGACTGAAGCCCGCTGGAGGCGCGCGCCAGGTGNAAGCGC 1950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 580 GGTAAGATTTCTTTATTACAGATATCGGAATGGCCACAGAGAGTGGAGAGCCCTTT 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1951 GCCTATGACCCGCTCCTGGACGTGGCAGCTTCGACCGGCCCGCGGTGGAGGCTGTGTG 2010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 CAGGGGCCCTGCACTGAATGGGAGCAAGACCTGCAGGAGC 682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2011 AAGCGGCCAGGAGCGCATGGGCATCGAGGCCGACGAGGAGG 2053
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 15
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194
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Query Match          3.2%; Score 40.6; DB 3; Length 21295;
Best Local Similarity 48.9%; Pred. No. 3.1;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 460 GTGCCCTCGGAGACGAGGCGCTGCAGGGCAACCCATGAAGCTGCGTGCATCTCCTGC 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2609 GTGCTGGAAGAGTGGAGCGCGCTGGCCGAGCTGGCGCTGATGCCCGGAGGCCGCGC 2668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 520 ATGAAGAGAGAGGAGTGGAGGCCACACGCTGCTGGAATGTTCTACAGGCCCGAGGGC 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2669 ATGGCTACGCGCAGAGCTGAAGCCCGCTGGAGGCGCGCGCCAGGTGAAGCGC 2728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 580 GGTAAGATTTCTTTATTACAGTATCGGAATGGCCACAGGAGTGGAGAGCCCTTT 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2729 GCCTATGACCCGCTCCTGGACGTGGCAGCTTCGACCGGCCGCGGTGGAGGCTGTGTG 2788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 640 CAGGGGCGCTCAGTGGAAATGGCAAGGACCTGCAGGACG 682
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2789 AAGCGGCCAGGAGCGCATGGGCATCGAGGCCGACGAGGAGG 2831
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: December 13, 2005, 07:35:09
Job time : 295.5 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:13:57 ; Search time 1440 Seconds
(without alignments)
7241.448 Million cell updates/sec

Title: US-09-977-579A-4
Perfect score: 1261
Sequence: 1 cctcccttcgagctgagc.....tgcagaactgagaagccgg 1261

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:
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3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	1259.4	99.9	1261	9	US-10-482-834A-22
3	600	47.6	600	10	US-11-060-756-2816
4	600	47.6	600	10	US-11-060-756-2817
5	600	47.6	600	10	US-11-060-756-7088
6	600	47.6	600	10	US-11-060-756-7089
7	561.8	44.6	1195	9	US-10-450-763-22568
8	559.6	44.4	2632	5	US-10-029-191-22
9	559.6	44.4	3108	5	US-10-023-191-1
10	540	42.8	2220	3	US-09-977-579-3
11	534.6	42.4	645	5	US-10-029-191-21
12	416	33.0	651	4	US-09-925-065A-513769
13	415.6	33.0	651	4	US-09-925-065A-513767
14	415.6	33.0	651	4	US-09-925-065A-513768
15	392.6	31.1	3531	9	US-10-450-763-22567
16	229.2	18.2	545	4	US-09-925-065A-774904
17	224.4	17.8	621	9	US-10-450-763-22566
18	216	17.1	4625	3	US-09-764-891-7659
19	148.2	11.8	657	5	US-10-029-191-23
20	143.8	11.4	1275	10	US-11-060-756-3901
21	143.8	11.4	1275	10	US-11-060-756-8173
22	143.8	11.4	1335	8	US-10-723-860-2247
23	142.2	11.3	1414	8	US-10-477-272-1
24	142.2	11.3	1414	9	US-10-482-834A-11
25	142.2	11.3	1414	9	US-10-482-834A-12
26	141	11.2	407	7	US-10-276-774-718
27	138.6	11.0	1490	3	US-09-917-800A-1654
28	87	6.9	496	4	US-09-925-065A-807954
29	87	6.9	502	4	US-09-925-065A-807996
30	86	6.8	495	4	US-09-925-065A-778585
31	81.4	6.5	807	6	US-10-401-916-12
32	81.4	6.5	974	6	US-10-401-916-13
33	49	3.9	243	6	US-10-029-386-16214
34	49	3.9	569	8	US-10-029-386-2514
35	48.6	3.9	3583	8	US-10-723-860-6471
36	45.4	3.6	876	7	US-10-767-701-10747
37	45.4	3.6	1645	9	US-10-647-517-29
38	45.2	3.6	497	7	US-10-424-599-133788
39	45.2	3.6	954	8	US-10-425-115-100998
40	44.8	3.6	921	6	US-10-369-493-43050
41	44.8	3.6	29340	7	US-10-322-281-642
42	44	3.5	53	9	US-10-491-192-5
43	44	3.5	60	9	US-10-491-192-6
44	43.8	3.5	1434	6	US-10-259-194A-622
45	43.8	3.5	1720	7	US-10-425-114-19213

RESULT 1

US-09-977-579-4

; Sequence 4, Application US/09977579

; Publication No. US20040248240A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod

; TITLE OF INVENTION: channel

; FILE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/977,579

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60,129,473

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-977-579-4

Query Match 100.0%; Score 1261; DB 3; Length 1261;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTCTGGGCGCAAAACGAGCGAGCGAGCGCGGAGTGG 60

Db 1 CCCTCCCTTCGAGCTGAGCTTACCTCTGGGCGCAAAACGAGCGAGCGAGCGCGGAGTGG 60

Qy 61 AAGCTGAGTTCGGGGTGGGGGAGGCGGAGTGTCCGTGGTGTCTGAGCCCGCGGAGA 120

Db 61 AAGCTGAGTTCGGGGTGGGGGAGGCGGAGTGTCCGTGGTGTCTGAGCCCGCGGAGA 120

Qy 121 GCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTCGGGGAGGTCAGTGGGGTTCGCTTAG 180

Db 121 GCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTCGGGGAGGTCAGTGGGGTTCGCTTAG 180

Qy 181 GGCCCAAGCCCCCAGCCCGGCTCCAAAGTCTCCAGGGCTCCCGAGGACACCGGTGCTCG 240

Db 181 GGCCCAAGCCCCCAGCCCGGCTCCAAAGTCTCCAGGGCTCCCGAGGACACCGGTGCTCG 240

Qy 241 GCCCTTCGTTGGTTCAGAAAGTCCCGCTGGGGGAGTTCGTTCCCAAGGGTTTCCTCG 300

Db 241 GCCCTTCGTTGGTTCAGAAAGTCCCGCTGGGGGAGTTCGTTCCCAAGGGTTTCCTCG 300

ALIGNMENTS

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Db 241 GCCCTTCTCGGTTCAGAAAGTCGCCCTCGGGGCGAGTTCTGTCCTCCAAAGAGGTTTCTCTCG 300
Qy 301 AAAGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAGC 360
Qy 361 CGCCAGCCCCAGAAAGATCCCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTGTGTCT 420
Db 361 CGCCAGCCCCAGAAAGATCCCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTGTGTCT 420
Qy 421 ATCTACTGGGTCAAGTCTGTCTTCCCTGTGTGTGTGGAAGTGCCTCGGAGACGAGGCC 480
Db 421 ATCTACTGGGTCAAGTCTGTCTTCCCTGTGTGTGTGGAAGTGCCTCGGAGACGAGGCC 480
Qy 481 GTGAGGCAACCCATCAAGCTGGCTGCATCTCTGCATGAAGAGAGAGAGGTGGAG 540
Db 481 GTGAGGCAACCCATCAAGCTGGCTGCATCTCTGCATGAAGAGAGAGAGGTGGAG 540
Qy 541 GCCACCAAGTGGTGGAAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAT 600
Db 541 GCCACCAAGTGGTGGAAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAT 600
Qy 601 GAGTATCGGAATGGCCACAGAGGTGAGAGGCCCTTTCAGGGGCGCTCGAGTGGAA 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGAGAGGCCCTTTCAGGGGCGCTCGAGTGGAA 660
Qy 661 GGCAGCAGGACCTGCAGAGCGTGCATCACTGTCTCAACGTCACCTCTGAAACGACTCT 720
Db 661 GGCAGCAGGACCTGCAGAGCGTGCATCACTGTCTCAACGTCACCTCTGAAACGACTCT 720
Qy 721 GGCTCTACACTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGATCGGCCCTTTGTG 780
Db 721 GGCTCTACACTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGATCGGCCCTTTGTG 780
Qy 781 AAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGTGAGAGGACTTCACTCT 840
Db 781 AAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGTGAGAGGACTTCACTCT 840
Qy 841 GTGGTCTCAGAAATCATGATGATATCTTCTGTGCTTTCCTCACCTGTGCTCTCATC 900
Db 841 GTGGTCTCAGAAATCATGATGATATCTTCTGTGCTTTCCTCACCTGTGCTCTCATC 900
Qy 901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAAACGCG 960
Db 901 GAGATGATATATTTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGCCCAAGAAAACGCG 960
Qy 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
Db 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
Qy 1021 TAGACAGGAGCGTGTGACATGAGTGGCTGACACCTGAGGACCTGGACATCCCATG 1080
Db 1021 TAGACAGGAGCGTGTGACATGAGTGGCTGACACCTGAGGACCTGGACATCCCATG 1080
Qy 1081 TTACGCAATGTCAATGGCATCAGAGGGCGGCCCAAGGGGCCCATCGCTTCCCTTCATGC 1140
Db 1081 TTACGCAATGTCAATGGCATCAGAGGGCGGCCCAAGGGGCCCATCGCTTCCCTTCATGC 1140
Qy 1141 ATCCATTTGTTCTGTTTCATTCATTCATCATATCCACTGCCCTGTGAGCTTTCACTCT 1200
Db 1141 ATCCATTTGTTCTGTTTCATTCATTCATCATATCCACTGCCCTGTGAGCTTTCACTCT 1200
Qy 1201 GACTCCCTAACTCCATCAGACTCTACCGCACCATAAGACTTGGCCAGAACTGAGAGCGC 1260
Db 1201 GACTCCCTAACTCCATCAGACTCTACCGCACCATAAGACTTGGCCAGAACTGAGAGCGC 1260
Qy 1261 G 1261
Db 1261 G 1261
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RESULT 2

US-10-482-834A-22

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; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Biomedics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-482-834A-22
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Query Match 99.9%; Score 1259.4; DB 9; Length 1261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTTGGCGCAAAACGAGCGAGCGAGGGCGCGAGTGG 60
Db 1 CCCTCCCTTCGAGCTGAGCTTACCTTGGCGCAAAACGAGCGAGCGAGGGCGCGAGTGG 60
Qy 61 AAGCTGAGTTCGGGGTGGCGGGAGGCGACTGTCCTGCTGCTGAGCCCGCGGAGGAGA 120
Db 61 AAGCTGAGTTCGGGGTGGCGGGAGGCGACTGTCCTGCTGCTGAGCCCGCGGAGGAGA 120
Qy 121 GCGGGCGGAGCGGCTGATCGGCTCCCTGAACTGGGGAGGTCAGTGGGGTCCCTTAG 180
Db 121 GCGGGCGGAGCGGCTGATCGGCTCCCTGAACTGGGGAGGTCAGTGGGGTCCCTTAG 180
Qy 181 GGCCCAAAGCCCCCACCCGGCTCCAAAAGTCCCAAGGGCTCCCAAGGACCGGTGTCG 240
Db 181 GGCCCAAAGCCCCCACCCGGCTCCAAAAGTCCCAAGGGCTCCCAAGGACCGGTGTCG 240
Qy 241 GCCCTTCCTTCGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCCAAAGGTTTCC 300
Db 241 GCCCTTCCTTCGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCCAAAGGTTTCC 300
Qy 301 AAAGAACTCGAGAGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAACTCGAGAGGCGCAGTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Qy 361 CGCCAGCCCCAGAAAGATGCTGCTTCCCTTCAATAGATTGTTTCCCTGGCTTCTCTGTG 420
Db 361 CGCCAGCCCCAGAAAGATGCTGCTTCCCTTCAATAGATTGTTTCCCTGGCTTCTCTGTG 420
Qy 421 ATCTACTGGGTCAAGTCTGTCTTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCC 480
Db 421 ATCTACTGGGTCAAGTCTGTCTTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCC 480
Qy 481 GTGAGGCAACCCATCAAGCTGCCTGCAATCTCTGCATGAAGAGAGAGAGGTGGAG 540
Db 481 GTGAGGCAACCCATCAAGCTGCCTGCAATCTCTGCATGAAGAGAGAGAGGTGGAG 540
Qy 541 GCCACCAAGTGGTGGAAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAT 600
Db 541 GCCACCAAGTGGTGGAAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAT 600
Qy 601 GAGTATCGGAATGGCCACAGAGGTGAGAGGCCCTTTCAGGGGCGCTCGAGTGGAA 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGAGAGGCCCTTTCAGGGGCGCTCGAGTGGAA 660
Qy 661 GGCAGCAGGACCTGCAGAGCGTGCATCACTGTCTCAACGTCACCTCTGAAACGACTCT 720
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Db 661 GGCAGCAGGACCTGCGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCT 720
Qy 721 GGCCTCTACACCTGCAATGTGTCCCGGAGTTCAGATTGTAGGGCGCATCGGCCCTTTGTG 780
Db 721 GGCCTCTACACCTGCAATGTGTCCCGGAGTTCAGATTGTAGGGCGCATCGGCCCTTTGTG 780
Qy 781 AAGACGACGGCGGTGATCCCTTAAGAGTCAACGAGGAGGCTGAGAGGACTTCACCTCT 840
Db 781 AAGACGACGGCGGTGATCCCTTAAGAGTCACTGAGGAGGCTGAGAGGACTTCACCTCT 840
Qy 841 GTGCTCTCAGAAATCATGATGTACATCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Db 841 GTGCTCTCAGAAATCATGATGTACATCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 900
Qy 901 GAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAAAAGCG 960
Db 901 GAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAAAAGCG 960
Qy 961 TCTGACTACCTTGCATCCCATCTAGAAACAAGAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
Db 961 TCTGACTACCTTGCATCCCATCTAGAAACAAGAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
Qy 1021 TAGAACGAGGACGTGTGACATGAGTGGCTGTGAACACCTGAGGACTTGGACATCCCATG 1080
Db 1021 TAGAACGAGGACGTGTGACATGAGTGGCTGTGAACACCTGAGGACTTGGACATCCCATG 1080
Qy 1081 TTGAGCAATGTCAATGGCATCAGAGGCGGCCCAAGGGCCCCATCGCTTCCCTTTCATGC 1140
Db 1081 TTGAGCAATGTCAATGGCATCAGAGGCGGCCCAAGGGCCCCATCGCTTCCCTTTCATGC 1140
Qy 1141 ATCCATTGTTCTGTTCAATTCATCATACATCCACCTGCTGAGCTTTTCACTCT 1200
Db 1141 ATCCATTGTTCTGTTCAATTCATCATACATCCACCTGCTGAGCTTTTCACTCT 1200
Qy 1201 GACTCCCTTAACCTCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAGCGG 1260
Db 1201 GACTCCCTTAACCTCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAGCGG 1260
Qy 1261 G 1261
Db 1261 G 1261
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RESULT 3
US-11-060-756-2816
; Sequence 2816, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2816
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2816

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Query Match 47.6%; Score 600; DB 10; Length 600;  
Best Local Similarity 100.0%; Pred. No. 6.5e-176;  
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 662 GCAGCAAGGACCTGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG 721  
Db 1 GCAGCAAGGACCTGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAGGACTCTG 60  
Qy 722 GCCTCTACACCTGCAATGTGTCCCGGAGTTCAGTTTGTAGGGCGCATCGGCCCTTTGTGA 781
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Db 61 GCCTCTACACCTGCAATGTGTCCCGGAGTTCAGTTTGTAGGGCGCATCGGCCCTTTGTGA 120  
Qy 782 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTTGGAGAGGACTTCACCTCTG 841  
Db 121 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTTGGAGAGGACTTCACCTCTG 180  
Qy 842 TGGTCTCAGAAATCATGATGTACATCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTATCG 901  
Db 181 TGGTCTCAGAAATCATGATGTACATCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTATCG 240  
Qy 902 AGATGATATATTGCTCAGAAAGGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAAAAGCGGT 961  
Db 241 AGATGATATATTGCTCAGAAAGGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAAAAGCGGT 300  
Qy 962 CTGACTACCTTGGCATCCCATCTGAGAAACAAGAGAGAACTCTGCGGTACCAAGTGGAGAA 1021  
Db 301 CTGACTACCTTGGCATCCCATCTGAGAAACAAGAGAGAACTCTGCGGTACCAAGTGGAGAA 360  
Qy 1022 AGAACAGGAGCAGTGTGACATGAGTGGCTGTGAACACCTGAGGAGCTTGGACATCCCATGT 1081  
Db 361 AGAACAGGAGCAGTGTGACATGAGTGGCTGTGAACACCTGAGGAGCTTGGACATCCCATGT 420  
Qy 1082 TCAGCAATGTCAATGGCATCAGAGGCGGCCCAAGGGCCCCATCGCTTCCCTTTCATGCA 1141  
Db 421 TCAGCAATGTCAATGGCATCAGAGGCGGCCCAAGGGCCCCATCGCTTCCCTTTCATGCA 480  
Qy 1142 TCATTGTTCTGTTCAATTCATTCATCATACATCCACCTGCTTCCCTTTCATGCTCTG 1201  
Db 481 TCATTGTTCTGTTCAATTCATTCATTCATCATACATCCACCTGCTTCCCTTTCATGCTCTG 540  
Qy 1202 ACTCCCTTAACCTCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAGCGG 1261  
Db 541 ACTCCCTTAACCTCAGACCTCTAGCACCATAAGACTCTGCCAGAACTGAGAGCGG 600
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RESULT 4
US-11-060-756-2817
; Sequence 2817, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817

```
Query Match 47.6%; Score 600; DB 10; Length 600;  
Best Local Similarity 100.0%; Pred. No. 6.5e-176;  
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 662 GCAGCAAGGACCTGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG 721  
Db 1 GCAGCAAGGACCTGAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAGGACTCTG 60  
Qy 722 GCCTCTACACCTGCAATGTGTCCCGGAGTTCAGTTTGTAGGGCGCATCGGCCCTTTGTGA 781  
Db 61 GCCTCTACACCTGCAATGTGTCCCGGAGTTCAGTTTGTAGGGCGCATCGGCCCTTTGTGA 120  
Qy 782 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTTGGAGAGGACTTCACCTCTG 841  
Db 121 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTTGGAGAGGACTTCACCTCTG 180  
Qy 842 TGGTCTCAGAAATCATGATGTACATCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTATCG 901
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Db 181 TGGTCTCAGAAATCATGATGTACATCTCTTCTGGTCTTCTCACCTGTGGTGTCTCATCG 240
Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 300
Qy 962 CTGACTACCTTGGCCATCCCATCTCAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
Db 301 CTGACTACCTTGGCCATCCCATCTCAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCA 1141
Db 421 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCA 480
Qy 1142 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 600

RESULT 5
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088

Query Match 47.6%; Score 600; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 6.5e-176;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 60
Qy 722 GCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 120
Qy 782 AGACGACGGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 841
Db 121 AGACGACGGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 180
Qy 842 TGGTCTCAGAAATCATGATGTACATCTTCTGGTCTTCTCACCTGTGGTGTCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCTTCTGGTCTTCTCACCTGTGGTGTCTCATCG 240
Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 300
Qy 962 CTGACTACCTTGGCCATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021

Db 301 CTGACTACCTTGGCCATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCA 1141
Db 421 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCA 480
Qy 1142 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATTCATCCATACATCCACCTGCTCTGAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCCACCATAGACTCTGCCAGAACTGAGAAGCGGG 600

RESULT 6
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Query Match 47.6%; Score 600; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 6.5e-176;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTG 60
Qy 722 GCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGCGCATCGGCCCTTTGTGA 120
Qy 782 AGACGACGGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 841
Db 121 AGACGACGGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTTCACCTCTG 180
Qy 842 TGGTCTCAGAAATCATGATGTACATCTTCTGGTCTTCTCACCTGTGGTGTCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCTTCTGGTCTTCTCACCTGTGGTGTCTCATCG 240
Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCCCAAGAAACCGGT 300
Qy 962 CTGACTACCTTGGCCATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
Db 301 CTGACTACCTTGGCCATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGGTGGCTTGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGCA 1141

Db	421	TCAGCAATGCAATGGGCATCAGGAGGGCGCCCAAGGGCCCATCGGTTCCCTTCATG6CA	480
Qy	1142	TCCATTGTTCTGTTTCATTTCATTATCCATATACATCCACCTGCGCTCTGAGCTTTTCACCTCTG	1201
Db	481	TCCATTGTTCTGTTTCATTTCATTATCCATATACATCCACCTGCGCTCTGAGCTTTTCACCTCTG	540
Qy	1202	ACTCCCTTAACTCCATTCAGACCTCTTACGCAACATTAAGACTCTGCGAGAACTGAGAAAGCGGG	1261
Db	541	ACTCCCTTAACTTCATTCAGACCTCTTACGCAACCATTAAGACTCTGCGAGAACTGAGAAAGCGGG	600

RESULT 7

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US-10-450-763-22568
; Sequence 22568, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hvaeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22568
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (518)..(1051)
; OTHER INFORMATION: 91% homologous to Homo sapiens voltage-gated sodium channel
; OTHER INFORMATION: beta-3 subunit, accession number AU243396, Smith-Waterman Score=826
US-10-450-763-22568

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Query Match	44.6%	Score 561.8;	DB 9;	Length 1195;
Best Local Similarity	95.8%	Pred. No. 6.6e-164;		
Matches 599;	Conservative	0;	Mismatches 22;	Indels 4;
			Gaps	2;

349	Qy	AGCCTTGGAGCGCCGACGCCAGAGATGCCTGCCTTCAATAGTTGTTTCCCTCGCT	408
436	Db	AGCCTTGGAGCGCCGACGCCAGAGATGCCTGCCTTCAATAGATTGTTTCCCTCGCT	495
409	Qy	TCTCTGTGCTTATCTACTCTGGTCAGTGTCTGCTTCCCTGTGTGTGTGGAA - GTGCGCT	466
496	Db	TCTCTGTGCTTATCTACTGAGTCAGTGTCTGCTTCCCTGTGTGGGGGAAAGTGCCTT	555
467	Qy	CGGAGACGGAGCGCGTGCA - GGGCAACCCCATGAAGTCGCGCTGCATCTCTCGCATGAA	524
556	Db	AGAAAA CGGGGGCGGCACGGGCTAACCCCATGAAGCTGCGCTGCATCTCTCGCATGAA	615
525	Qy	GAGAGAGAGGTGGAGGCCACACCGTGTGTGGAAATGTTCTACAGGCCCGAGGGCGGTAA	584
616	Db	GAGAGAGAGGTGGAGGCCACACCGTGTGTGGAAATGTTCTACAGGCCCGAGGGCGGTAA	675
585	Qy	AGATTTCTTTATTTACGAGTATCGGAATGGCCACACGAGAGGTGAGAGAGCCCTTTTCAGGG	644
676	Db	AGATTTCTTTATTTACGAGTATCGGAATGGCCACACGAGAGGTGAGAGAGCCCTTTTCAGGG	735
645	Qy	GCGCCTGCAGTGGAAATGGCAGCAAGGACCTGCAGGACGTGTCCATCATGTGCTCAACGT	704
736	Db	GCGCCTGCAGTGGAAATGGCAGCAAGGACCTGCAGGACGTGTCCATCATGTGCTCAACGT	795
705	Qy	CACCTCTGAA CGACTCTGGCTCTACACCTGCAATGTGTCCCGGAGATTGTGATTTGAGGC	764
796	Db	CACCTCTGAA CGACTCTGGCTCTACACCTGCAATGTGTCCCGGAGATTGTGATTTGAGGC	855

Qy	765	GCATCGGCCCTTTGTGTAAGACGACGGCGTGTATCCCCCTAAGAGTCACCGAGGAGGCTGG	824
Db	856	GCATCGGCCCTTTGTGAAGACGACGGCGGTGATCCCCCTAAGAGTCACCGAGGAGGCTGG	915
Qy	825	AGAGGACTTCACCTCTCTGTGTCACAGAAATCATGATGTACATCCTCTTGTTCTTCCTCAC	884
Db	916	AGAGGACTTCACCTCTCTGTGTCACAGAAATCATGATGTACATCCTCTTGTTCTTCCTCAC	975
Qy	885	CCTGTGCTGCTCATCGAGATGATATATTGCTACAGAAAGGTCTCAAAGCCGAAGAGGC	944
Db	976	CTTGTGCTGCTCATCGAGATGATATATTGCTACAGACAGGTCTCAAAAGCCGAAGAGGC	1035
Qy	945	AGCCCAAGAAAAACGGTCTGACTAC	969
Db	1036	AGCCCAAGAAAAACGGCCAGGAAAC	1060

RESULT 8

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US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

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Query Match	44.4%	Score 559.6;	DB 5;	Length 2632;
Best Local Similarity	84.4%	Pred. No. 4.2e-163;		
Matches 655; Conservative	0;	Mismatches 114;	Indels 7;	Gaps 2;

Qy	371	AGAAGATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGCTTATCTACTCTGGG	430
Db	73	AAAAGATGCCTGCCTTCAACAGATTGTTTCCCTAGCTTCTTAGTGCTCATCTACTCTGGG	132
Qy	431	TCAGTGTCTGTTCCCTGTGTGTGTGAAGTGCCCTCGGAGACGGAGGCCGTGCAGGGCA	490
Db	133	TCAGAGTCTGTTCCCTGTGTGTGTGNAAGTGCCCTCGGAGACAGAAAGCGGTGCAGGGCA	192
Qy	491	ACCCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAGGAGGTGGAGGCCACCACGG	550
Db	193	ATCCCATGAAGCTGAGGTGCATCTCTCTGCATGAAGAGGGAGGAGGTGGAGGCCACCACGT	252
Qy	551	TGTTGGAAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCTTATTTACGAGTATCGGA	610
Db	253	TGTTGGAGTGGTTCTACAGGCCCTGAGGGCGGTAAAGATTTCTTATATATAGAGTATCGGA	312
Qy	611	ATGGCCACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAGTGGAAATGGCAGCAAGG	670
Db	313	ATGGCCACCAGGAAGTGGAGAGCCCTTTTCAGGCCCTCTGCAGTGGAAATGGGAGCAAG	372
Qy	671	ACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCCCTTACA	730
Db	373	ACCTGCAGGACGTATCCATCACTGTACTCAATGTCACTTTGAAATGACTCTGGCCCTTACA	432
Qy	731	CCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAAGACGACGC	790
Db	433	CATGCAATGTGTCCAGGAGTTTCGAATTCAGGGCACACAGGCCCTTTGTGNAAGACCAGA	492
Qy	791	GGCTGTATCCCCCTAAAGAGTCACCGAGGAGGTGGAGAGGACTTCACCTCTGTGTGCTTCAG	850

Db 538 TGGTGGAGTGGTCTACAGGCGCTGAGGCGGTAAAGATTTCTTATATATAGTATCGGA 597
Qy 611 ATGGCCACAGGAGTGGAGAGCCCTTTCAAGGGCGCTCGAGTGGAAATGGCAGCAAG 670
Db 598 ATGGCCACAGGAGTGGAGAGCCCTTTCAAGGGCGCTCGAGTGGAAATGGGAGCAAG 657
Qy 671 ACCTGCAGGAGTGCATCATCTGCTCAAGCTCACTCTGAACGACTCTGGCTCTTACA 730
Db 658 ACCTGCAGGAGTATCCATCATCTGCTCAATGTCACTTTGAATGACTCTGGCTCTACA 717
Qy 731 CCTGCAATGTCTCCGGGAGTTTGAAGTGGAGGCGCATCGGCCCTTTGTGAAGACGAGC 790
Db 718 CATGCAATGTCTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTGTGAAGACGAGC 777
Qy 791 GGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTGTGTCTCAG 850
Db 778 GACTGATACCTTTGCGAGTCACTGAAGAGGCGGAGAGACTTCACTCTCGTGTCTCGG 837
Qy 851 AAATCATGATGATACATCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 910
Db 838 AAATCATGATGATACATCTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 897
Qy 911 ATTGCTACAGAAAGTCTCAAAAGCCGAAGAGGAGGCGCCCAAGAAACGCGTCTGACTACC 970
Db 898 ATTGCTACAGAAAGTCTTAAAGCCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 957
Qy 971 TTGCTATCCCTTCAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1022
Db 958 TTGCTATCCCTTCAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1009

RESULT 11

US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

Query Match 42.4%; Score 534.6; DB 5; Length 645;
Best Local Similarity 89.3%; Pred. No. 1.6e-155;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 376 ATGCTGCTCAATAGATTTGTTCCCTGCTTCTCTGCTGCTTCTTCTGCTGCTTCTGCTGCT 435
Db 1 ATGCTGCTCAACAGATTTCTTCCCTGCTTCTTCTGCTGCTTCTTCTGCTGCTTCTGCTGCT 60
Qy 436 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGAGCGAGGCGGTGCGAGGCAACCC 495
Db 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGAGCGAGGCGGTGCGAGGCAATCCC 120
Qy 496 ATGAAGCTGCTGCATCTCTGCTGATGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 555
Db 121 ATGAAGCTGAGTGCATCTCTGCTGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180
Qy 556 GAATGGTCTTACAGGCGCGGCGGTAAAGATTTCTTATTTAGAGATTCGGAATGGC 615
Db 181 GAGTGGTCTTACAGGCGCGGCGGTAAAGATTTCTTATATATAGATTCGGAATGGC 240

Qy 616 CACCAGAGGTGGAGAGCCCTTTCAAGGGCGCTCGAGTGGAAATGGCAGCAAGACCTG 675
Db 241 CACCAGAGGTGGAGAGCCCTTTCAAGGGCGCTCGAGTGGAAATGGGAGCAAGACCTG 300
Qy 676 CAGGAGCTGTCCATCACTGTCTCAAGCTCACTCTGAACGACTCTGGCTCTTACACCTGC 735
Db 301 CAGGAGCTGTCCATCACTGTCTCAAGCTCACTCTGAACGACTCTGGCTCTTACACATGC 360
Qy 736 AATGTGTCGGGAGTTTGAAGTGGAGGCGCATCGGCCCTTTGTGAAGACGAGCGGCTG 795
Db 361 AATGTGTCGGGAGTTTGAAGTGGAGGCGCACAGGCCCTTTGTGAAGACGAGGACTG 420
Qy 796 ATCCCTTAAAGATCAACGAGGAGGCTGGAGAGACTTCACTCTGTGTGTCTCAGAAATC 855
Db 421 ATACCTTTGGAGTCACTGAAGAGGCGGAGAGACTTCACTCTCGTGTCTCGAAATC 480
Qy 856 ATGATGTACATCTTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 915
Db 481 ATGATGTACATCTTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
Qy 916 TACAGAAAGTCTCAAAAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975
Db 541 TACAGAAAGTCTTAAAGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Qy 976 ATCCATCTGAGAAACAGGAGAACTCTTGGGTACCGTACCGTGGAGGAA 1020
Db 601 ATCCCTTCAGAGAAACAGGAGAACTCTTGGGTACCTGTGGAGGAA 645

RESULT 12

US-09-925-065A-513769
; Sequence 513769, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957085
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513769
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513769

Query Match 33.0%; Score 416; DB 4; Length 651;
Best Local Similarity 99.8%; Pred. No. 1.4e-118;
Matches 427; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CTCCCTTCCAGCTGAGCTTACCTGGCGCGCAACGAGCGAGGCGGCGGAGTGGAA 62
Db 131 CTCCCTTCCAGCTGAGCTTACCTGGCGCGCAACGAGCGA-GCAGGCGCGGAGTGGAA 189
Qy 63 GCTGAGTTCGGGGTGGGGGAGGAGCGACTGTCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 122
Db 190 GCTGAGTTCGGGGTGGGGGAGGAGCGACTGTCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGT 249
Qy 123 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTTCCAGTGGGGTGTGCTTAGGG 182

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Db      250 GGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCGCTTAGGG 309
Qy      183 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 242
Db      310 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 369
Qy      243 CTTCTCTCGGTGAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAAAGGGTTTCTCGAA 302
Db      370 CTTCTCTCGGTGAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAAAGGGTTTCTCGAA 429
Qy      303 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 362
Db      430 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 489
Qy      363 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 422
Db      490 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 549
Qy      423 CTACTGGG 430
Db      550 CTACTGGG 557
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RESULT 13

```
US-09-925-065A-513767
; Sequence 513767, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513767
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513767
```

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Query Match      33.0%; Score 415.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.8e-118;
Matches 426; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      3 CTCCCTTCGAGCTGAGCTTACCTTGGGGGCAAAACGAGGAGCGAGGGCGCGAGTGAA 62
Db      131 CTCCCTTCGAGCTGAGCTTACCTTGGGGGCAAAACGAGGAGCGAGTGAA 189
Qy      63 GCTGGAGTTCCGGGTGGGGGAGGCGACTGTCGTGTGCTGAGCGCGCGAGAGC 122
Db      190 GCTGGAGTTCCGGGTGGGGGAGGCGACTGTCGTGTGCTGAGCGCGCGAGAGC 249
Qy      123 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGG 182
Db      250 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGG 309
Qy      183 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 242
Db      310 CCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 369
Qy      243 CTTCTCTCGGTGAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAAAGGGTTTCTCGAA 302
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Db      370 CTTCTCTCGGTGAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAAAGGGTTTCTCGAA 429
Qy      303 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 362
Db      430 AGAATCTGAGAGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 489
Qy      363 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 422
Db      490 CCAGCCCCAGAGATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTAT 549
Qy      423 CTACTGGG 430
Db      550 CTACTGGG 557
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RESULT 14

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US-09-925-065A-513768
; Sequence 513768, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513768
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513768
```

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Query Match      33.0%; Score 415.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.8e-118;
Matches 426; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

```
Qy      3 CTCCCTTCGAGCTGAGCTTACCTTGGGGGCAAAACGAGGAGCGAGGGCGCGAGTGAA 62
Db      131 CTCCCTTCGAGCTGAGCTTACCTTGGGGGCAAAACGAGGAGCGAGTGAA 189
Qy      63 GCTGGAGTTCCGGGTGGGGGAGGCGACTGTCGTGTGCTGAGCGCGCGAGAGC 122
Db      190 GCTGGAGTTCCGGGTGGGGGAGGCGACTGTCGTGTGCTGAGCGCGCGAGAGC 249
Qy      123 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGG 182
Db      250 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGG 309
Qy      183 CCCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 242
Db      310 CCCAAAGCCCCACCGGCTCCAAAGCTCCAGGGCTCCCAAGGACCGGTGCTCGGC 369
Qy      243 CTTCTCTCGGTGAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAAAGGGTTTCTCGAA 302
Db      370 CTTCTCTCGGTGAGAAAGTCCGCCCTGGGGGAGTTCGTCCTCAAAAGGGTTTCTCGAA 429
Qy      303 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 362
Db      430 AGAATCTGAGAGGCGCAGTCTTTGACCGAGGGAATCTCTGTGTAGCCCTTGAAGCCG 489
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Job time : 1444 secs

Qy 363 CCAGCCCAAGATGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTCGTCTTAT 422
Db 490 CCAGCCCAAGATGCTGCTTCAATAGATTGTTTCCCTGCTTCTCTCGTCTTAT 549
Qy 423 CTACTGGG 430
Db 550 CTACTGGG 557

RESULT 15
US-10-450-763-22567
; Sequence 22567, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22567
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (300)..(407)
; OTHER INFORMATION: 94% homologous to Homo sapiens putative kruppel-related zinc
; OTHER INFORMATION: finger protein NY-REN-23 antigen, accession number AF155101, Smith-
; OTHER INFORMATION: Waterman Score=180.
US-10-450-763-22567

Query Match 31.1%; Score 392.6; DB 9; Length 3531;
Best Local Similarity 99.0%; Pred. No. 4.8e-111;
Matches 395; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 422 TCTACTGGTCAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGGAGCCG 481
Db 2951 TCAGGTGTGTCAAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCGGAGACGGAGCCG 3010
Qy 482 TGCAGGGCAACCCCATGAAGCTGCGTGCATCTCTGCTGATGAAGAGAGAGGTGGAGG 541
Db 3011 TGCAGGGCAACCCCATGAAGCTGCGTGCATCTCTGCTGATGAAGAGAGAGGTGGAGG 3070
Qy 542 CCACACGGTGGTGGAAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCCTTATTTACG 601
Db 3071 CCACACGGTGGTGGAAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCCTTATTTACG 3130
Qy 602 AGTATCGGAATGGCCACAGAGAGTGGAGACCCCTTTTCAGGGCGCGCTGCAGTGGAAATG 661
Db 3131 AGTATCGGAATGGCCACAGAGAGTGGAGACCCCTTTTCAGGGCGCGCTGCAGTGGAAATG 3190
Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGTCACTGTGAACGACTCTG 721
Db 3191 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAAGTCACTGTGAACGACTCTG 3250
Qy 722 GCCTCTACCTGCAATGTGTCCGGGAGTTTGAAGTTTGAGGGCGCATCGGCCCTTTGTGA 781
Db 3251 GCCTCTACCTGCAATGTGTCCGGGAGTTTGAAGTTTGAGGGCGCATCGGCCCTTTGTGA 3310
Qy 782 AGACGACGGCGCTGATCCCCCTAAGAGTCAACCGAGGAGG 820
Db 3311 AGACGACGGCGCTGATCCCCCTAAGAGTCAACCGAGGAGG 3349

Search completed: December 13, 2005, 14:31:24

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Qy 241 GCCCTTCTTCGGTTCAGAAAGTCGCCCTCGGGGGCAGTTGCTCCCAAGGGTTTCCTCG 300
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Qy 241 GCCCTTCTTCGGTTCAGAAAGTCGCCCTCGGGGGCAGTTGCTCCCAAGGGTTTCCTCG 300
Db |||||
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Db |||||
Qy 301 AAAGAAATCTGAGAGGGCGCAGTCTCTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAGC 360
Db |||||
Qy 361 CGCAGAGCCCAAGATGCTCGCTTCAATAGATTGTTCCCTCGGCTTCTCTCGTCTT 420
Db |||||
Qy 361 CGCAGAGCCCAAGATGCTCGCTTCAATAGATTGTTCCCTCGGCTTCTCTCGTCTT 420
Db |||||
Qy 421 ATCTACTGGGTTCAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Db |||||
Qy 421 ATCTACTGGGTTCAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Db |||||
Qy 481 GTGCAAGGCCAACCCATGAGCTCGCTGTCATCTCTGCAATGAAGAGAGAGGAGGTGGAG 540
Db |||||
Qy 481 GTGCAAGGCCAACCCATGAGCTCGCTGTCATCTCTGCAATGAAGAGAGAGGAGGTGGAG 540
Db |||||
Qy 541 GCCACCAAGTGTGGAAATGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTATTAC 600
Db |||||
Qy 541 GCCACCAAGTGTGGAAATGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTATTAC 600
Db |||||
Qy 601 GAGTATCGGAATGCCACAGAGGTGGAGAGCCCTTTCAAGGGCGCTGCACTGGAAT 660
Db |||||
Qy 601 GAGTATCGGAATGCCACAGAGGTGGAGAGCCCTTTCAAGGGCGCTGCACTGGAAT 660
Db |||||
Qy 661 GGCAAGCAAGGACCTGCAAGAGCTGTCATCACTGTGCTCAACGTCACCTGGAAGACTCT 720
Db |||||
Qy 661 GGCAAGCAAGGACCTGCAAGAGCTGTCATCACTGTGCTCAACGTCACCTGGAAGACTCT 720
Db |||||
Qy 721 GGCCTCTACACTGCAATGTGTCCGGAGTTTGAGTTTGAGGGCGATCGGCCCTTTGTG 780
Db |||||
Qy 721 GGCCTCTACACTGCAATGTGTCCGGAGTTTGAGTTTGAGGGCGATCGGCCCTTTGTG 780
Db |||||
Qy 781 AAGACGAGCGGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGAGAGGACTTCACCTCT 840
Db |||||
Qy 781 AAGACGAGCGGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGAGAGGACTTCACCTCT 840
Db |||||
Qy 841 GTGCTCTCAGAAATCATGATGTACATCCTCTGCTGCTTCTCCTCACCTGTGCTCATC 900
Db |||||
Qy 841 GTGCTCTCAGAAATCATGATGTACATCCTCTGCTGCTTCTCCTCACCTGTGCTCATC 900
Db |||||
Qy 901 GAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAAACGG 960
Db |||||
Qy 901 GAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAAACGG 960
Db |||||
Qy 961 TCTGACTACCTTGGCATCCCATCTGAGAAACAGAGAACTCTGCGGTACCACTGGAGGAA 1020
Db |||||
Qy 961 TCTGACTACCTTGGCATCCCATCTGAGAAACAGAGAACTCTGCGGTACCACTGGAGGAA 1020
Db |||||
Qy 1021 TAGAACAGGACAGTGTGACATGAGGTGGCTGAAACACCTGAGGAGCTGGACATCCCATG 1080
Db |||||
Qy 1021 TAGAACAGGACAGTGTGACATGAGGTGGCTGAAACACCTGAGGAGCTGGACATCCCATG 1080
Db |||||
Qy 1081 TTGAGCAATGTCAATGGCATCAGAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Db |||||
Qy 1081 TTGAGCAATGTCAATGGCATCAGAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Db |||||
Qy 1141 ATCCATTGTTCTGTTTCATTTCATTCATCATATCCACCTGCTGAGCTTTTCACTCT 1200
Db |||||
Qy 1141 ATCCATTGTTCTGTTTCATTTCATTCATCATATCCACCTGCTGAGCTTTTCACTCT 1200
Db |||||
Qy 1201 GACTCCCTTAACTCCATCAGACTCTTACGCAACCAAGAACTCTGCGAGAACTGAGAAGCG 1260
Db |||||
Qy 1201 GACTCCCTTAACTCCATCAGACTCTTACGCAACCAAGAACTCTGCGAGAACTGAGAAGCG 1260
Db |||||
Qy 1261 G 1261
Db 1261 G 1261
```

```
RESULT 2
US-10-374-954-4
; Sequence 4, Application US/10374954
; Publication No. US2005026057eA1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(681)
US-10-374-954-4

Query Match      11.4%; Score 143.8; DB 6; Length 1335;
Best Local Similarity 56.9%; Pred. No. 1.3e-30;
Matches 334; Conservative 0; Mismatches 232; Indels 21; Gaps 3;

Qy 441 CTTCCCTGTGTGTGGAAAGTGCCCTCGAGACGGAGGCGGTGAGGCAACCCCATGAA 500
Db 75 CTGGGGGGTGTGCTGAGAGTGGACTCGGAGACGAGGCGGTGTATGGGTGACTTCAA 134
Qy 501 GCTGCGCTGCACTCTCTGCATGAAGAGAGAGGAGGTGGAGGCCACCGGTGGGAATG 560
Db 135 AATTCTTTTGATCTCTCTGCAAGCGCCGAGCGACCAACGCTGAGACCTTCAACGAGTG 194
Qy 561 GTTCTACAGGCCCGGCGGTAAAGATT-----TCCTTATTTACGAGTATCGAA 611
Db 195 GACCTTCCGCGAGAAAGGCGCATGAGGAGTTTGTCAAGATCCTGCGCTATGAGAATGAGGT 254
Qy 612 TGGCCACACGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGGGAATGGCAG----- 665
Db 255 GTTCACGCTGGAGAGAGTGAAGCGCTTCGAGGGCGCGTGGTGGGAATGGCAGCGGGG 314
Qy 666 ---CAAGGACCTGCAGAACGTTGCCATCACTGTGCTCAACGTCACTCTGAAACGACTTGG 722
Db 315 CACCAAGACCTGCAGGATCTGTCTATCTTCATCAACCAATGTCACTACCAACCACTCGGG 374
Qy 723 CTTCTACACCTGCAATGTGTCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAA 782
Db 375 CGACTACAGTGCACGCTTACCGCCTGCTCTTCGAAACTTCAGAGCAACACCCAG 434
Qy 783 GACGACGCGGTGATCCCTCAAGAGTCACCGAGAGGCTGGAGAGGACTTCACCTCTGT 842
Db 435 CGTGTCAAGAGATCACATTTAGGTAGTGGACAAGGCCAACAGAGACATGGCATCCAT 494
Qy 843 GGTCTCAGAAATCATGATGATCATCTTCTGTGGTCTTCTTCAACCTGTGGTGTCTCATGA 902
Db 495 CGTGTCTGAGATCATGATGATGTGCTCATTTGGTGTGTGACCATATATGGCTTCGTGGCAGA 554
Qy 903 GATGATATTTGCTACAGAAAGGTCTCAAAGCCGAAGAG---CGACCCCAAGAAAACGC 959
Db 555 GATGATTTACTGTCTACAGAAAGATCGCTGCGCCGACCGAGAGACTGCTGCACAGGAGAAATGC 614
Qy 960 GTCTGACTTACCTTCCCATCCCATCTGAGAAACAGGAGAACTCTCTGCGG 1006
Db 615 CTGGAATACCTGGCCATCACCTCTGAAGCAAGAGAACTGACGG 661

RESULT 3
US-10-750-185-44336
```



```
; LENGTH: 193789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-55

Query Match          4.0%; Score 51; DB 7; Length 193789;
Best Local Similarity 58.1%; Pred. No. 0.00072;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 441 CTTCCCTGTGTGTGGAGTGCCTCGGAGACGGAGCGCGTGCAGGCAACCCCATGAA 500
Db 102787 CTGGGGGGCTGCGTGGAGGTGGACTCGGAGACCGAGGCCGTGTATGGATGACCTTCAA 102846

Qy 501 GCTCGCTGTCATCTCTCATGAAGAGAGAGAGGTGGAGGCCACCAACGCTGAGACCTTACCGAGTG 560
Db 102847 AATCTTTGCAATCTCTCAAGCGCGCGAGGAGACCAACGCTGAGACCTTACCGAGTG 102906

Qy 561 GTTCTACAGGCCGAGGCGGTAAAGATTTCCTTA 595
Db 102907 GACCTTCGCCAGAGGGCACTGAGGAGTTTGTC A 102941

RESULT 7
US-11-121-086-61/c
; Sequence 61, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 169495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (70072)..(70171)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (139457)..(157244)
; OTHER INFORMATION: a, c, g, t, unknown or other
US-11-121-086-61

Query Match          3.6%; Score 44.8; DB 7; Length 169495;
Best Local Similarity 56.7%; Pred. No. 0.037;
Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy 74 GGGTGGCGGGGAGCGCACTGTCGTGCTGAGCGCCGCGAGAGCGGCGCGAGC 133
Db 45491 GGGAGGGCGGTAGGGACCTTTCAGAGCAGAGGGGCTTTCCGGGGCGGTGGGGCGCGC 45432

Qy 134 GCGTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCG-CTTAGGGGCCAAAGCCC 192
Db 45431 TCGGAGCGGAGCGCGGCTCGACGCGGTGCGCTGCGGCGAGTGTATGAGACGGGCG 45372

Qy 193 CCACCGCGCTCAAAAGCTCCAGAGGCGCTCCAGGCAACCGGTGCTGGCGCTTCCCTTCG 252
Db 45371 CGGGCCCGAAACCCGAGCCCGCGGGGCTCCCGACCGCGGCGCTCCCGCGCCCTCCCGCG 45312

RESULT 8
US-10-770-726-27
; Sequence 27, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27

Query Match          3.2%; Score 40.2; DB 6; Length 2838;
Best Local Similarity 49.8%; Pred. No. 0.14;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 23 ACCTGGGCGCAACAGCAGCGAGCGGGGCGCGAGTGGAGCTTCCGGGGTGGC 82
Db 577 ACCAGGCCAGAGGGGCCCCAGGAGGAGGAGCCGAGCGCGTTCGCCCGTCAAGC 636

Qy 83 GGGGAGCGCACTGTCTCCGTGTGTGTAGCGCGCGCGAGCGGGCGCGAGCGGTGATCG 142
Db 637 GAGCGGGTGGCGCACTGTGTACAGGCGAGCGGGGCGCGAGAGAGAGGCCCAAGTCT 696

Qy 143 GTCCTCTGAACTGGGAGGTCCAGTGGGTGCGTTAGGGCCCAAGCCCCCAGCCCGCT 202
Db 697 TCCAGGAGGGGCTCAGGGGGTCCCGAGGAGTCTCTCCCGGAGCAACGCCCTCTCCGGG 756

Qy 203 CCAAAAGCTCCAGGGCTCCCCAG 227
Db 757 CTTGATGTCGGCACCCCCAGCCTG 781

RESULT 9
US-10-750-185-46989
; Sequence 46989, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46989
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Bovine
; ORGANISM: Bovine 19866880829104
US-10-750-185-46989

Query Match          3.1%; Score 39; DB 6; Length 1931;
Best Local Similarity 52.8%; Pred. No. 0.27;
Matches 84; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 54 CGAGTGAAGCTGGAGTTCCGGGGTGGCGGAGGCGACTGTCCGTGGTCTCAGCGCC 113
Db 1745 CGAGAGGCCCCCTGGAGTCAACCACTTCATGGGGGCAAGCTGCCACCGCGCTCTGCACG 1804

Qy 114 GCGAGAGCGGGCGCGAGCGGTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGT 173
Db 114 GCGAGAGCGGGCGCGAGCGGTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGT 173
```


Db 1805 AAGAGGAACAGGGTCAGAGCTGGAGATGGGATCAACACAGGCGCCCTAGGTACAGTAGGCC 1864

Qy 174 CGCTTAGGGCCCAAGGCCCCACCCGGCTCCAAAAGTTC 212

Db 1865 CTCTGAGACCTGGAGAGCCCTCCCGGCTTCATACCCCC 1903

RESULT 10
US-10-507-928-9
; Sequence 9, Application US/10507928
; Publication No. US20050266024A1
; GENERAL INFORMATION:

```

, , APPLICANT: POWDERMED LIMITED AND GLAXO GROUP LIMITED
, ,
, , FILE OF INVENTION: ADJUVANT
, ,
, , TITLE REFERENCE: N.88232B GCW
, ,
, , CURRENT APPLICATION NUMBER: US/10/507,928
, ,
, , CURRENT FILING DATE: 2004-09-17
, ,
, , NUMBER OF SEQ ID NOS: 12
, ,
, , SOFTWARE: PatentIn version 3.1
, ,
, , SEQ ID NO 9
, ,
, , LENGTH: 1689
, ,
, , TYPE: DNA
, ,
, , ORGANISM: Artificial sequence
, ,
, , FEATURE:
, ,
, , OTHER INFORMATION: nucleotide sequence of RT insert
, ,
, , US-10-507,928-9

```

Query Match	3.0%;	Score 38;	DB 6;	Length 1689;
Best Local Similarity	62.8%;	Pred. No. 0.4%;		
Matches 59;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;

Qy	623	AGTGTGAGAGCCCTTTACAGGGGCGCTTGCAAGTGGATGGCAGCAGGACCTCGAGGACG	682
Db	278	AGCTGGGATCCCCCATCCGCGCGCTTGAAGAAGAGAGCGTGACCGTCTGGACG	337
Qy	683	TGTCATCACTGTGCTCAACGCTCACTCTGAACGA	716
Db	338	TGGCGCAGCGTTACTTTCAGCCCTCCCTCTGGACGA	371

RESULT 11
US-10-507-328-11
; Sequence 11, Application US/10507928
; Publication No. US2005026602A1
; GENERAL INFORMATION:

```

, GENERAL INFORMATION:
, APPLICANT: POWDERED LIMITED AND GLAXO GROUP LIMITED
, TITLE OF INVENTION: ADJUVANT
, FILE REFERENCE: N.89232B GCW
, CURRENT APPLICATION NUMBER: US/10/507,928
, CURRENT FILING DATE: 2004-09-17
, NUMBER OF SEQ ID NOS: 12
, SOFTWARE: PatentIn version 3.1
, SEQ ID NO 11
, LENGTH: 1689
, TYPE: DNA
, ORGANISM: Artificial sequence
, FEATURE:
, OTHER INFORMATION: nucleotide sequence of the coding
US-10-507-928-11

```

	Query Match	3.0%	Score 38;	DB 6;	Length 1689;
	Best Local Similarity	62.8%;	Pred. No. 0.49;		
	Matches 59;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;
Qy	623	AGTTGGAGAGCCCCCTTTTCAGGGGGCGCTTCAGTGGAAATGGCAGACGAGCACTCTGACGACG	682		
Db	278	AGCTGGGCATCCCCCATCCGCGCGSCTTGAAGAGAGAGAGCGTGACCTGCTGGACG	337		
Qy	683	TGTCATCACTGTGCTCAACGTCACCTCTGAACGA	716		
Db	338	TGGGCGAGCGCTTACTTTCAGCCCTCCCTCTGGACGA	371		

RESULT 12
US-11-029-465-9
; Sequence 9, Application US/11029465
; Publication No. US20050256070A1
; GENERAL INFORMATION:

```

1 APPLICANT: Inoué, Shinya
2 APPLICANT: Van-Wely, Catherine
3 APPLICANT: Ertl, Peter
4 APPLICANT: Adjuvant
5 TITLE OF INVENTION:
6 FILE REFERENCE: 033267-015
7 CURRENT APPLICATION NUMBER: US/11/029,465
8 CURRENT FILING DATE: 2005-01-06
9 NUMBER OF SEQ ID NOS: 12
10 SOFTWARE: FastSEQ for Windows Version 4.0
11 SEQ ID NO 9
12 LENGTH: 1689
13 TYPE: DNA
14 ORGANISM: Artificial Sequence
15 FEATURE:
16 OTHER INFORMATION: nucleotide sequence of
17 US-11-029-465-9

```

Query Match	3.0%	Score 38;	DB 7;	Length 1689;
Best Local Similarity	62.8%	Pred. No. 0.49;		
Matches 59;	Conservative 0;	Mismatches 35;	Indels 0;	Gaps 0;

Qy	623	AGTGGAGAGCCCTTTTCAGGGGGGCTTCAGCTGGGAATGGCACAGGACCTCGAGGACG	682
Db	278	AGCTGGGCATCCCCATCCGCGGCGCTGAAGAAGAAGAGCGTGACCGTGTGGACG	337
Qy	683	TGTCCTCATCTGTGCTCAACGTCACCTGAACGA	716
Db	338	TGGCGCAGCGTTTACTTCAGGCTCCCTCTGGACGA	371

RESULT 13
US-11-029-465-11
; Sequence 11, Application US/11029465
; Publication No. US20050256070A1

```

; GENERAL INFORMATION:
; APPLICANT: Braun, Ralph P.
; APPLICANT: Thomsen, Lindy
; APPLICANT: Van-Wely, Catherine
; APPLICANT: Ertl, Peter
; TITLE OF INVENTION: Adjuvant
; FILE REFERENCE: 033267-015
; CURRENT APPLICATION NUMBER: US/11/029,465
; CURRENT FILING DATE: 2005-01-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1689
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of the coding insert in
; US-11-029-465-11

```

	Query Match	3.0%;	Score 38;	DB 7;	Length 1689;
	Best Local Similarity	62.8%;	Pred. No. 0.49;		
	Matches	59;	Conservative	0;	Mismatches 35; Indels 0; Gaps 0;
Qy	623	AGTGGAGAGCCCTTTACAGGGGGCGCTGCAGCTGGGAATGCAGCAGGACCTGCAGGACG	682		
Db	278	AGCTGGCATCCCGCCCGCGCTGAAGAAGAGAGCGTGACCGTGTGGACG	337		
Qy	683	TGTCCATCATTGTGCTCAACGTCACCTGAACGA	716		
Db	338	TGGCGGACGGTTACTTCAGGGTCCCTCTGGACGA	371		

Job time : 345 secs

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RESULT 14
US-11-121-086-29/c
; Sequence 29, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; TYPE: DNA
; LENGTH: 160226
; ORGANISM: Homo sapiens
US-11-121-086-29

Query Match      3.0%; Score 37.8; DB 7; Length 160226;
Best Local Similarity 52.2%; Pred. No. 3.2;
Matches 84; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY      49 GGGCGCGAGTGGAGCTGGAGTTCGGGGTGGGGGGGAGGCGACTGTCCGTGGTGTGA 108
      |||||
Db      141257 GGCACGCGGGCGGGCGGGCGGGCGGAGGCGGGCGCGGCGGCGGCGGCGGCGG 141198

QY      109 GCGCGCGGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 168
      |||||
Db      141197 GGGAGCGGTGGAGGGGCTGGGGAGGAGGAAGGACGTCAGGGGAGGGGGCGGCGAGGG 141138

QY      169 GGGGTGCGCTTAGGGGCCAAAGCCCCCACCCTCCGGCTCCAAAAG 209
      |||||
Db      141137 CGGGCGCGCGGACCGCCGCCCGCCCGCGCGCCCTTAAAG 141097

RESULT 15
US-11-121-086-62
; Sequence 62, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; TYPE: DNA
; LENGTH: 200628
; ORGANISM: Homo sapiens
US-11-121-086-62

Query Match      3.0%; Score 37.8; DB 7; Length 200628;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY      1128 CTTCCCTTCATGCATCCATGTTGTTTCATTCATTCATCATCATCCACTGCCTCTG 1187
      |||||
Db      163254 CATCCATCCATCCATCCATCCATCTATCCATTCGTCATCCATCCATTCACCTACTATCC 163313

QY      1188 AGCTTTACCTCTGACTCCCTAACTCCATCCAGACCTCAGGCACC 1232
      |||||
Db      163314 ATCCATATCCATTCATTCATCCACCCATCCTCATTCATCCATC 163358
```

Result No.	Score	Query Match	Length	DB	ID	Description
C	1	44.8	11.9	11558	6	PCI-US93-06251-23 Sequence 23, Appl
	2	42	11.2	9822	3	US-09-949-016-15003 Sequence 15003, A
	3	41	10.9	1097	3	US-09-771-161A-58 Sequence 58, Appl
	4	41	10.9	3382	3	US-09-771-161A-59 Sequence 59, Appl
	5	40.4	10.8	6651	3	US-09-902-540-4944 Sequence 4944, Ap
	6	40.4	10.8	30780	3	US-09-902-540-1243 Sequence 1243, Ap
	7	40.2	10.7	2802	3	US-09-949-016-1335 Sequence 1335, Ap
	8	40.2	10.7	2806	3	US-09-688-188B-102 Sequence 102, App
	9	40.2	10.7	2806	3	US-09-291-417D-102 Sequence 102, App
	10	40.2	10.7	2838	3	US-09-949-016-794 Sequence 794, App
	11	40.2	10.7	57559	3	US-09-949-016-13077 Sequence 13077, A
	12	40.2	10.7	57560	3	US-09-949-016-12536 Sequence 12536, A
C	13	40	10.7	21295	3	US-09-902-540-1194 Sequence 1194, Ap
	14	39.2	10.5	601	3	US-09-949-016-124631 Sequence 124631, A
	15	39.2	10.5	8374	3	US-09-949-016-15257 Sequence 15257, A
	16	39.2	10.5	45225	3	US-09-949-016-12428 Sequence 12428, A
	17	39.2	10.5	45226	3	US-09-949-016-13654 Sequence 13654, A
	18	39	10.4	30635	3	US-09-949-016-16501 Sequence 16501, A
	19	39	10.4	43414	3	US-09-949-016-12839 Sequence 12839, A
	20	39	10.4	43415	3	US-09-949-016-16491 Sequence 16491, A
	21	38.8	10.3	1941	3	US-09-902-540-4762 Sequence 4762, Ap
	22	38.8	10.3	26492	3	US-09-902-540-1234 Sequence 1234, Ap
	23	38.6	10.3	1940	3	US-09-718-032-1 Sequence 1, Appli
	24	38.6	10.3	1941	3	US-09-082-737-1 Sequence 1, Appli

```
Db 428 GGGAGGGGCGGTAGGGACCTTTACAGACGAGGAGGGCTTTGGGGCGGTGGGGCGCGC 487
Qy 134 GCCTGATCGGCTCCTCGAACTGGGAGGTCCAGTGGGTG-CTTAGGGCCCAAGCCC 192
Db 488 TGGGAGCGGAGCGCGGCTCGAGCGGGTGCCTGTGGGGGAGTGTATGAGACGGCGC 547
Qy 193 CCACCGGCTCCAAAAGCTCCAGGGCTCCCGGAGGACCGGTGCTGGGCCCTTCCTTCG 252
Db 548 CCGGCGGAAACCGAGCGCGGGGCTCCACCGCGGCTCCCGGCCCTCCCGCG 607

RESULT 2
US-09-949-016-15003/c
; Sequence 15003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15003
; LENGTH: 9622
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15003

Query Match 11.2%; Score 42; DB 3; Length 9622;
Best Local Similarity 49.5%; Pred. No. 0.53;
Matches 108; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 38 GAGCGAGCAGGGCGGAGTGGAGTTCGGGGTGGGGGAGGCGACTGTC 97
Db 7138 GCGTGAGGCCCTGCTGGAAAGGGTCTGCTGCTGCGGTAGGGCTCTGTTCATGCCACGA 7079
Qy 98 CGTGTCTAGCGCCGCGAGAGCGGGCGGAGCGGCTATCGGCTCCCTCGAATGG 157
Db 7078 TCTGCTGCTGTGGTGGGCCAGCGCGGTGTAGGAAGCCATCATGCCCTCCATCGGCTGG 7019
Qy 158 GGAGTCCAGTGGGTGCTTTAGGGCCCAAGAGCCCCACCGGCTCCAAAAGCTCCCAAG 217
Db 7018 ACAGGACCTTGGGGGACAGTAGCCCTTACCCCTGCTGTGTCACGCGCTCCACG 6959
Qy 218 GCCTCCCGAGCAGCGGTGCTCGGCCCTTCCTTCGGTC 255
Db 6958 TACACCCAGCAGCCTCCCTTCTGATCTCTTGGAC 6921

RESULT 3
US-09-771-161A-58
; Sequence 58, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
```

```
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-58

Query Match 10.9%; Score 41; DB 3; Length 1097;
Best Local Similarity 52.0%; Pred. No. 0.75;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTTGGCGCAAAACAGCGAGGCGGCGAGTGG 60
Db 23 CCCCCGCTCGGGGCTGTAGCGGCTCGGGGCGGGGCTGGCGCGGTGCGCGGCGG 82
Qy 61 AAGCTGAGTTCGGGGTGGCGGGAGGAGGACTGTCCTGTTGCTGAGCGCGGCGAGA 120
Db 83 CCGACGCTCCTCTTCGGCGGCGGCGGCGGCGCATGCTGGGCGCGCGGCTGGGGCG 142
Qy 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTGCT 177
Db 143 GCGGGCGCGAGTTGCTCCCGGGGCGCGGCTGAGGGGCCCCCGCGCGCGCGCT 199

RESULT 4
US-09-771-161A-59
; Sequence 59, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: -
; LOCATION: (1)..(3382)
; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c', 'g' or 't'
US-09-771-161A-59

Query Match 10.9%; Score 41; DB 3; Length 3382;
Best Local Similarity 52.0%; Pred. No. 0.83;
Matches 92; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTTGGCGCAAAACAGCGAGGCGGCGAGTGG 60
Db 23 CCCCCGCTCGGGGCTGTAGCGGCTCGGGGCGGGGCTGGCGCGGTGCGCGGCGG 82
Qy 61 AAGCTGAGTTCGGGGTGGCGGGAGGAGTGTCCGTGTTGCTGAGCGCGCGGCGAGA 120
Db 83 CCGACGCTCCTCTTCGGCGGCGGCGGCGGCGCATGCTGGGCGCGCGGCTGGGGCG 142
Qy 121 GCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGTGCT 177
Db 143 GCGGGCGCGAGTTGCTCCCGGGGCGCGGCTGAGGGGCCCCCGCGCGCGCGCT 199

RESULT 5
US-09-902-540-4944
; Sequence 4944, Application US/09902540
```

Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4944
; LENGTH: 6651
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4944

Query Match 10.8%; Score 40.4; DB 3; Length 6651;
Best Local Similarity 51.3%; Pred. No. 1.2;
Matches 120; Conservative 0; Mismatches 111; Indels 3; Gaps 1;
Qy 39 AGCAGGAGGGGCGGAGTGGAGTGGAGTTCGGGGTGGGGGAGGCGACTGCC 98
Db 4498 ATCAGGAGGGGCGGCTCGAGGCGCGGTGTCGCGGACACGCGGATGAAGCACGGGGCC 4557
Qy 99 GTGGTGTGAGCGCGCGGAGAGCGGGCGGAGCGGTGATCGGCTCCCTCGAACTGGG 158
Db 4558 CTGGAGCTG---CTCTTCTGACCGCGCGTGCAGCGGTATGAGCGCCCTGTCGTGGCGAG 4614
Qy 159 GAGTCCAGTGGGTGCTTAGGGCCCAAGCCCGGCTCCAAAGCTCCCAAGG 218
Db 4615 GTGGAGCTGTGAGTCTGCTGATTGGCGCTGTGGGCCACGCGGTGCTGCATCCAATG 4674
Qy 219 CTTCCCGAGGACCGGTGCTCGGCGCTTCTTCGTGGTTCAGAAAGTCCGCGCCCTGG 272
Db 4675 TCGGGAGCTGTTTCGGCGGGGATGCTCAAGTCCATCGGGCGGGAAGTGCCTGCCCGG 4728

RESULT 6
US-09-902-540-1243
; Sequence 1243, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1243
; LENGTH: 30780
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(30780)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1243

Query Match 10.8%; Score 40.4; DB 3; Length 30780;
Best Local Similarity 51.3%; Pred. No. 1.4;
Matches 120; Conservative 0; Mismatches 111; Indels 3; Gaps 1;
Qy 39 AGCAGGAGGGGCGGAGTGGAGTTCGGGGTGGGGGAGGCGACTGCC 98
Db 28499 ATCAGGAGGGGCGGCTCGAGGCGCGGTGTCGCGGACACGCGGATGAAGCACGGGGCC 28558

Qy 99 GTGGTGTGAGCGCGCGGAGACGCGGCGGAGCGGCTGATCGGCTCCTCGAACTGGG 158
Db 28559 CTGGAGCTG---CTCTTCTTGTGACGCGCGGTGTCGCGCGCTGTCTCGTGGCGAG 28615
Qy 159 GAGTCCAGTGGGTGCTTAGGGCCCAAGCCCGGCTCCAAAGCTCCCAAGG 218
Db 28616 GTGGAGCTGGTGTGATGTCATTTGGCGTGTGGGCCCGACGCGGTGCTGCATCCAATG 28675
Qy 219 CTTCCCGAGGACCGGTGCTCGGCGCTTCTTCGTTCGTCAGAAAGTTCGCGCCCTGG 272
Db 28676 TCGGGAGCTGTTTCGGCGGGATGCTCAAGTCCATCGGGCGGGAAGTGCCTGCCCGG 28729

RESULT 7
US-09-949-016-1335
; Sequence 1335, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1335
; LENGTH: 2802
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1335

Query Match 10.7%; Score 40.2; DB 3; Length 2802;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
Qy 23 ACCCTGGGGCGCAAAACGAGCGAGGCGGCGCGAGTGGAGTTCGCGGGTGGGC 82
Db 569 ACCACGCGCAGAGGGGGGCCCGAGGAGGAGGAGGCGCGGTTTCGCGGTCACAGC 628
Qy 83 GGGAGGCGGACTGTCGTGTGTGTGAGCGCGCGGAGAGCGGGCGGAGGCGGCTGATCG 142
Db 629 GAGGCGGGTGGCGGCGAGTGTGTGACGCGGCGGCGGCGGAGAGAGGCGGCTCT 688
Qy 143 GCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGGGCCCAAGCCCCCGGCT 202
Db 689 TCAGGAGGCGGCTCAGGGGTCCCGAGGAGTCTCCCGGAGCAACACGCCCCCTCTCCGGG 748
Qy 203 CCAAAAGCTCCAGGGCTCCCGAG 227
Db 749 CCTGATGTCGGCACCCCGGAGCCTG 773

RESULT 8
US-09-688-188B-102
; Sequence 102, Application US/09688188B
; Patent No. 6656716
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0328
; CURRENT APPLICATION NUMBER: US/09/688,188B
; CURRENT FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 09/291,417

; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 102
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-688-188B-102

Query Match 10.7%; Score 40.2; DB 3; Length 2806;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGCGCAACGACGAGCGAGGCGGGCCGAGTGGAGCTGGAGTTCGGGGTGGGC 82
DB 567 ACCACGGCCAGAGGGGGCCAGGGAAGCAGCGACGCGCGGTTCGCGGTTCACAGC 626

QY 83 GGGGAGGCGACTGTCCTGGTGTCTGAGCGCGCGAGAGCGGGCGCGAGCGGCTGATCG 142
DB 627 GAGCGGGTGGCGCAGTGTGTACAGCGCAGCGGGCGCCAGAGAGAGGCCCAAGTCT 686

QY 143 GCTCCCTCGAACTGGGAGGTCCTAGTGGGTCTGCTTAGGGCCCAAGCCCCACCCGGCT 202
DB 687 TCCAGGAGGGCTCAGGGGGTCTCCAGGAGTCTCTCCGGGACAAACGCCCTCTCCGGG 746

QY 203 CCAAAAGCTCCAGGGCTCTCCCGAG 227
DB 747 CCTGATGTCCGACACCCCGCAGCCTG 771

RESULT 9

US-09-291-417D-102
; Sequence 102, Application US/09291417D
; Patent No. 6680170
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WHYTE, DAVID
; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 038602/0329
; CURRENT APPLICATION NUMBER: US/09/291,417D
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/081,784
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 102
; LENGTH: 2806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-291-417D-102

Query Match 10.7%; Score 40.2; DB 3; Length 2806;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCCTGGCGCAACGACGAGCGAGGCGGGCCGAGTGGAGCTGGAGTTCGGGGTGGGC 82
DB 567 ACCACGGCCAGAGGGGGCCAGGGAAGCAGCGACGCGCGGTTCGCGGTTCACAGC 626

QY 83 GGGGAGGCGACTGTCCTGGTGTCTGAGCGCGCGAGAGCGGGCGCGAGCGGCTGATCG 142
DB 627 GAGCGGGTGGCGCAGTGTGTACAGCGCAGCGGGCGCCAGAGAGAGGCCCAAGTCT 686

QY 143 GCTCCCTCGAACTGGGAGGTCCTAGTGGGTCTGCTTAGGGCCCAAGCCCCACCCGGCT 202
DB 687 TCCAGGAGGGCTCAGGGGGTCTCCAGGAGTCTCTCCGGGACAAACGCCCTCTCCGGG 746

QY 203 CCAAAAGCTCCAGGGCTCTCCCGAG 227
DB 747 CCTGATGTCCGACACCCCGCAGCCTG 771

RESULT 10

US-09-949-016-794
; Sequence 794, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 794
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-794

Query Match 10.7%; Score 40.2; DB 3; Length 2838;
Best Local Similarity 49.8%; Pred. No. 1.3;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 23 ACCTGGGCGCAACGACGAGCGAGGCGGGCGCGAGTGGAGCTTCGGGGTGGGC 82
DB 577 ACCACGGCCAGAGGGGGCCAGGGAAGCAGCGACGCGCGGTTCGCGGTTCACAGC 636

QY 83 GGGGAGGCGACTGTCCTGGTGTCTGAGCGCGCGAGAGCGGGCGCGAGCGGCTGATCG 142
DB 637 GAGCGGGTGGCGCAGTGTGTACAGCGCAGCGGGCGCGAGAGAGGCCCAAGTCT 696

QY 143 GCTCCCTCGAACTGGGAGGTCCTAGTGGGTCTGCTTAGGGCCCAAGCCCCACCCGGCT 202
DB 697 TCCAGGAGGGCTCAGGGGGTCTCCCGAGGAGTCTCTCCGGGACAAACGCCCTCTCCGGG 756

QY 203 CCAAAAGCTCCAGGGCTCTCCCGAG 227
DB 757 CCTGATGTCCGACACCCCGCAGCCTG 781

RESULT 11

US-09-949-016-13077
; Sequence 13077, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13077
; LENGTH: 57559
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13077

```

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-949-016-1194

Query Match          10.7%; Score 40; DB 3; Length 21295;
Best Local Similarity 47.9%; Pred. No. 1.7; Indels 0; Gaps 0
Matches 115; Conservative 0; Mismatches 125;

Qy 45 GCAGGGCGCGAGCTGGAAGCTCGAGTTCCGGGGTGGGGGAGGCGACTGTCCGTGGTG 104
Db 16255 GGAGGAGAGGCGCGTGCAGCGCATCCAGAGCTGCTCGAGGGGCGGGGGCGCGG 16314

Qy 105 CTGAGCGCCGCGAGAGCGGGCGCGAGCGGCTGTGATCGGCTCCCTCGAACTGGGAGGTC 164
Db 16315 CGCAGCGCGCCACGCCCGCGCGGAGCGCCGCCGAGGCACCCCGCTGGCGCGGG 16374

Qy 165 CAGTGGGTCGTTAGGCGCCAAAGCCCCACCCGGCTCCAAAAGCTCCAGGGCCTCCC 224
Db 16375 CTCGGCGGACGAGCTGCACGAAGCGGCCCTTTTCGCCACGGGCTCACGGTGGGAGCCT 16434

Qy 225 CAGGCACCGGTGCTCGGCCCTTCCTTCGGTCAGAAAAGTCGCCCCCTGGGGGCGAGTTCGTC 284
Db 16435 CAGGGCAGCGCTGAGCTGATCCAAAGCGTCGAAGGTGGCGCGCTGTAGCGCTCCGAC 16494

RESULT 14
US-09-949-016-124631
; Sequence 124631, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124631
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-124631

Query Match          10.5%; Score 39.2; DB 3; Length 601;
Best Local Similarity 48.2%; Pred. No. 1.9; Indels 0; Gaps 0
Matches 110; Conservative 0; Mismatches 118;

Qy 49 GGGCGCGAGTGAAGCTGGAGTTCCGGGGTGGGGGAGGCGACTGTCCTGGTCTGA 108
Db 84 GGAGTGGGTGCCCAAGGGGTCTGTGGGGTGCGAGAAGCGTCTCTCCCTCGACTCG 143

Qy 109 GCGCCGCGAGAGCGGGCGCGAGCGGTGTATCGGCTCCCTCGAACTGGGGAGGTCAGT 168
Db 144 GGGCGCCCGAGCGCTTGGCGGGTCTCCCGCTGAGCGGTGCGCGCTGCGCGCAGCCACTGCT 203

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49 GGGCGGAGTGGAGCTGAGTTCCTGGGGTGGCTGGGAGGCGATGCTCCCTGGTCTCTG 108
QY
84 GGGAGTGGGTGCCAAGGGGGTCTGGCGGGTGCAGAAAGCGTCTGCTCCCTCGGACTCG 143
Db
109 GCCCGGCGAGAGCGGGCGCGAGCGGTGATCGGCTCCCTCGAACTGGGAGAGTCCAGT 168
QY
144 GGGCGCCCGAGCCCTGGCGGGTCCCGCTGAGCGGCTGCCCTGCGCGCGACCACTGT 203
Db

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Qy 169 GGGGTGCTTAGGGCCCAAGCCCCACCGGCTCCAAAAGTCCAGGGCTCCCCAGG 228
Db 204 CACCTCCGGGGCGCTCGCCAGGCGGCCCTGCGTCCCGGGTCCCCCGGCTGCCAGG 263
Qy 229 CACCGGTGCTCGGCCCTTCTTCCGTCAGAAAGTCGCCCCCTGGGGGC 276
Db 264 GAGCGGAGTGGGTTCACAGCGGCCCGTGGCGCACKCCGGCTGGGC 311

RESULT 15
US-09-949-016-15257
; Sequence 15257, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15257
; LENGTH: 8374
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15257

Query Match 10.5%; Score 39.2; DB 3; Length 8374;
Best Local Similarity 48.2%; Pred. No. 2.5;
Matches 110; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

Qy 49 GGGCGCAGTGGAGCTGAGTTCGGGGTGGCGGGAGCGACTGTCCGTGTGCTGA 108
Db 5933 GGGAGTGGGTCCCCAAGGGGGTCTGTGGCGGTGGCAGAGCGTCTCCCCCTCGGACTCG 5992
Qy 109 GCGCGCGCAGAGCGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGT 168
Db 5993 GCGCGCCCAACCTTGGCGGGTCTCCCGCTGAGCGGCTGCCCGTCCCGCGGCTGCCAGT 6052
Qy 169 GGGGTGCTTAGGGCCCAAGCCCCACCGGCTCCAAAAGTCCAGGGCTCCCCAGG 228
Db 6053 CACCTCCGGGGCGCTCGCCAGGCGGCCCTGCGTCCCGGGTCCCCCGGCTGCCAGG 6112
Qy 229 CACCGGTGCTCGGCCCTTCTTCCGTCAGAAAGTCGCCCCCTGGGGGC 276
Db 6113 GAGCGGAGTGGGTTCACAGCGGCCCGTGGCGCACTCCGGCTGGGC 6160
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Search completed: December 13, 2005, 07:35:11
Job time : 88.9845 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	375	100.0	1261	3	US-09-977-579-4	Sequence 4, Appl
2	375	100.0	1261	9	US-10-482-834A-22	Sequence 22, Appl
3	361	96.3	651	4	US-09-925-065A-513769	Sequence 513769,
4	360.6	96.2	651	4	US-09-925-065A-513767	Sequence 513767,
5	360.6	96.2	651	4	US-09-925-065A-513768	Sequence 513768,
c 6	45.2	12.1	437	7	US-10-424-599-133788	Sequence 133788,
7	44.8	11.9	29340	7	US-10-322-281-642	Sequence 642, App
8	43	11.5	336	7	US-10-437-963-98256	Sequence 98256, A
c 9	43	11.5	1021	7	US-10-767-701-11876	Sequence 11876, A
c 10	42.6	11.4	419	8	US-10-425-115-24179	Sequence 24179, A
c 11	42.2	11.3	1211	7	US-10-437-963-27585	Sequence 27585, A
c 12	41.4	11.0	696	7	US-10-437-963-90177	Sequence 90177, A
c 13	41.4	11.0	58038	8	US-10-741-600-17942	Sequence 17942, A
14	41.4	11.0	333811	8	US-10-741-600-17681	Sequence 17681, A
15	41.2	11.0	922	6	US-10-017-161-1435	Sequence 1435, Ap
c 16	41.2	11.0	922	6	US-10-292-798-1161	Sequence 1161, Ap
17	41	10.9	1097	3	US-09-771-161A-58	Sequence 58, Appl
c 18	41	10.9	3382	3	US-09-771-161A-59	Sequence 59, Appl
c 19	40.2	10.7	766	7	US-10-260-238-52	Sequence 52, Appl
c 20	40.2	10.7	791	7	US-10-437-963-84059	Sequence 84059, A
c 21	40.2	10.7	1071	7	US-10-437-963-84064	Sequence 84064, A
c 22	40.2	10.7	2739	9	US-10-956-157-4971	Sequence 4971, Ap
c 23	40.2	10.7	2806	3	US-09-291-417-102	Sequence 102, App

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Db 241 GCCCTTCCTCGGTGAGAAAGTCGCCCTCGGGGCGAGTTCCGTCCCAAGGGTTTCCTCG 300
Qy 301 AAAGAATCTGAGAGGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGGAAGC 360
Db 301 AAAGAATCTGAGAGGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGGAAGC 360
Qy 361 CGCCAGCCCCAGAAG 375
Db 361 CGCCAGCCCCAGAAG 375

RESULT 2
US-10-482-834A-22
; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hillary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-22

Query Match 100.0%; Score 375; DB 9; Length 1261;
Best Local Similarity 100.0%; Pred. No. 9.5e-98;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCAGGAGCGAGGGCGCGAGTGG 60
Db 1 CCCTCCCTTCGAGCTGAGCTTACCCCTGGGGCGCAACAGCAGGAGCGAGGGCGCGAGTGG 60
Qy 61 AAGCTGAGATTCGCGGGTGGCGGGGAGCGACTGTCGTTGCTGAGCGCCGCGGAGA 120
Db 61 AAGCTGAGATTCGCGGGTGGCGGGGAGCGACTGTCGTTGCTGAGCGCCGCGGAGA 120
Qy 121 GCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTGCCTTAG 180
Db 121 GCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTGCCTTAG 180
Qy 181 GCGCCAAAGCCCCACCGCGGCTCCAAAGCTCCAGAGGCGCTCCCGAGGCACCGGTGCTCG 240
Db 181 GCGCCAAAGCCCCACCGCGGCTCCAAAGCTCCAGAGGCGCTCCCGAGGCACCGGTGCTCG 240
Qy 241 GCCCTTCCTTCGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCCAAGGGTTTCCTCG 300
Db 241 GCCCTTCCTTCGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCCAAGGGTTTCCTCG 300
Qy 301 AAAGAATCTGAGAGGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGGAAGC 360
Db 301 AAAGAATCTGAGAGGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGGAAGC 360
Qy 361 CGCCAGCCCCAGAAG 375
Db 361 CGCCAGCCCCAGAAG 375

RESULT 3
US-09-925-065A-513769
; Sequence 513769, Application US/09925065A
```

```
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 513769
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513769

Query Match 96.3%; Score 361; DB 4; Length 651;
Best Local Similarity 99.7%; Pred. No. 1e-93;
Matches 372; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CTCCTTCCTCGAGCTGAGCTTACCCCTGGGCGCAACAGCAGGAGCGAGGGCGCGAGTGGAA 62
Db 131 CTCCTTCCTCGAGCTGAGCTTACCCCTGGGCGCAACAGCAGGAGCGAGGGCGCGAGTGGAA 189
Qy 63 GCTGAGTTCGCGGGTGGGCGGGAGCGAGCTGCTCCGTGTGTGCTGAGCGCCGCGGAGAGC 122
Db 190 GCTGAGTTCGCGGGTGGGCGGGAGCGAGCTGCTCCGTGTGTGCTGAGCGCCGCGGAGAGC 249
Qy 123 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCTAGGG 182
Db 250 GGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCTAGGG 309
Qy 183 CCCTAAAGCCCCACCGCGGCTCCAAAGCTCCCGAGGCGCTCCCGAGGCACCGGTCTCGGC 242
Db 310 CCCTAAAGCCCCACCGCGGCTCCAAAGCTCCCGAGGCGCTCCCGAGGCACCGGTCTCGGC 369
Qy 243 CTTTCCTTCGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCCAAGGGTTTCTCGAA 302
Db 370 CTTTCCTTCGGTTCAGAAAGTCCGCCCTGGGGGAGTTCGTCCCAAGGGTTTCTCGAA 429
Qy 303 AGAATCTGAGAGGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGCG 362
Db 430 AGAATCTGAGAGGGCGCAGTCCCTTGACCGAGGGAATCTCTGTGTAGCTTTGGAAGCG 489
Qy 363 CCAGCCCCAGAAG 375
Db 490 CCAGCCCCAGAAG 502

RESULT 4
US-09-925-065A-513767
; Sequence 513767, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
```

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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513767
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513767

Query Match          96.2%; Score 360.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.3e-93;
Matches 371; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CTCCTTCCGAGCTGAGCTTACCTCGGGCGCAACGAGCGAGGCGGGCGCGAGTGGAA 62
Db 131 CTCCTTCCGAGCTGAGCTTACCTCGGGCGCAACGAGCGAGGCGGGCGCGAGTGGAA 189

Qy 63 GCTGGAGTTCCGGGGTGGGGGAGCGACTGTCCTGCTGCTGAGCGCGGGCGAGAGC 122
Db 190 GCTGGAGTTCCGGGGTGGGGGAGCGACTGTCCTGCTGCTGAGCGCGGGCGAGAGC 249

Qy 123 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTCGGTTAGGG 182
Db 250 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTCGGTTAGGG 309

Qy 183 CCCAAAGCCCCCAGCCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACCGGTCCTCGGC 242
Db 310 CCCAAAGCCCCCAGCCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACCGGTCCTCGGC 369

Qy 243 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCTGCCAAAGGGTTTCTCGAA 302
Db 370 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCTGCCAAAGGGTTTCTCGAA 429

Qy 303 AGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTGTGTAGCTTGGAGCCG 362
Db 430 AGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTGTGTAGCTTGGAGCCG 489

Qy 363 CCAGCCCCAGAG 375
Db 490 CCAGCCCCAGAG 502

RESULT 5
US-09-925-065A-513768
; Sequence 513768, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513768
; LENGTH: 651
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-513768

Query Match          96.2%; Score 360.6; DB 4; Length 651;
Best Local Similarity 99.5%; Pred. No. 1.3e-93;
Matches 371; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 3 CTCCTTCCGAGCTGAGCTTACCTCGGGCGCAACGAGCGAGGCGGGCGCGAGTGGAA 62
Db 131 CTCCTTCCGAGCTGAGCTTACCTCGGGCGCAACGAGCGAGGCGGGCGCGAGTGGAA 189

Qy 63 GCTGGAGTTCCGGGGTGGGGGAGCGACTGTCCTGCTGCTGAGCGCGGGCGAGAGC 122
Db 190 GCTGGAGTTCCGGGGTGGGGGAGCGACTGTCCTGCTGCTGAGCGCGGGCGAGAGC 249

Qy 123 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTCGGTTAGGG 182
Db 250 GGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCAGTGGGGTCGGTTAGGG 309

Qy 183 CCCAAAGCCCCCAGCCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACCGGTCCTCGGC 242
Db 310 CCCAAAGCCCCCAGCCCGGCTCCAAAGCTCCAGGGGCTCCCAAGGACCGGTCCTCGGC 369

Qy 243 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCTGCCAAAGGGTTTCTCGAA 302
Db 370 CCTTCTTCGGTCAGAAAGTCGCCCCCTGGGGGAGTTCTGCCAAAGGGTTTCTCGAA 429

Qy 303 AGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTGTGTAGCTTGGAGCCG 362
Db 430 AGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTGTGTAGCTTGGAGCCG 489

Qy 363 CCAGCCCCAGAG 375
Db 490 CCAGCCCCAGAG 502

RESULT 6
US-10-424-599-133788/c
; Sequence 133788, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 133788
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(497)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_91816C.1
US-10-424-599-133788

Query Match          12.1%; Score 45.2; DB 7; Length 497;
Best Local Similarity 54.6%; Pred. No. 0.0033;
Matches 89; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 38 GAGCGAGGCGGGCGCGAGTGGAAAGTGGAGTTCCGGGGTGGGGGAGGCGGACTGTGTC 97
Db 301 GGGGGGGGAGGGGGGGGGGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 242

Qy 98 CGTGGTGTGAGCGCCCGCGAGAGCGGGCGCGGAGCGGGCTGTGCTCCCTCGAACTGG 157
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; SEQ ID NO 24179

; LENGTH: 419

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(419)

; OTHER INFORMATION: unsure at all n locations

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_122057C.1

US-10-425-115-24179

Query Match 11.4%; Score 42.6; DB 8; Length 419;

Best Local Similarity 51.7%; Pred. No. 0.019;

Matches 119; Conservative 0; Mismatches 110; Indels 1; Gaps 1;

Qy 56 AGTGAAGCTGAGTTCGGGGTGGCGGGAGCGACTGTCCGTGCTGTGAGCGCGG 115

Db 371 AGTCTAGCGCGGAGAGTGGGTGCTGCTTTCGAGCGGGGGGGGG 312

Qy 116 CGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTCG 175

Db 311 GGAGACCGAGCGGAAGCGGGCGGCGAGCACTGTCTGTGGGCGAGGCCAGCCCCCGC 252

Qy 176 CTTAGAGCCCAAGACCCCGCTCCAAAAGCTCCAGGGCTCCCGAGCACCGGT 235

Db 251 TGGAGGCCCGCACCGGCGAGGAGCAGCGGAGCGGCCCGCGAGGGGCGAGGA 192

Qy 236 GCTCGGCCCT-TCCCTTCGGTCAGAAAGTCGCCCGCTCGGGGCGAGTTCGTC 284

Db 191 GCTTAGCGANGTCCGCGGCCAGTAGGACTCGGCCCTTGAGGTTGGCCGCC 142

RESULT 11

US-10-437-963-27585/c

; Sequence 27585, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 27585

; LENGTH: 1211

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_32265C.1

US-10-437-963-27585

Query Match

Best Local Similarity 11.3%; Score 42.2; DB 7; Length 1211;

Matches 80; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

Qy 40 GCGAGGCGAGGGCGGAGTGAAGCTCGAGTTCGGGGTGGCGGGAGCGAGCGACTGTCCG 99

Db 204 GCGGCGGGGGGGGGGGGGGGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 145

Qy 100 TGGTGTGAGCGCGCGGCGAGAGCGGGCGCGAGCGGCTGATCCCTCGAACTGGGG 159

Db 144 GGGGCGGGCGCGCGGG 85

Qy 160 AGGTCCAGTGGGGTTCGCTTAGG 182

Db 84 GGGCGCGCGGGGGCGCGGGGG 62

RESULT 12

US-10-437-963-90177/c

; Sequence 90177, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 90177

; LENGTH: 696

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_88871C.1

US-10-437-963-90177

Query Match 11.0%; Score 41.4; DB 7; Length 696;

Best Local Similarity 48.5%; Pred. No. 0.04;

Matches 114; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Qy 10 CCGAGCTGAGCTTACCTTGGGCGCAACGAGCGAGGCGGGGCGCGAGTGAAGCTGGAG 69

Db 594 CGGCGGGCGCGACCGAGCGCGGGATGCGAGCGCGGCGGAGGTGGCCCGTGC 535

Qy 70 TTCGGGGTGGCGGGAGCGGACTGTCCGTGTGTGTGAGCGCGCGGAGAGCGGGCGCG 129

Db 534 GGTGAGCGCCAGCGGGCGCGCGCGGCGGCGGAGGCGCGGCGGCGGAGAGCGCCGTC 475

Qy 130 GAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTCGTTAGGGCCCAAG 189

Db 474 GAGCGCAACAGCGCGCGCGGGGATGCGTGTGGGGCCCACTGTCCGGGCCG 415

Qy 190 CCCCCACCGGCTCCAAAAGCTCCAGGGCTCCCGAGGCGCCCGGAGGCGCGGCGCC 244

Db 414 TCCCTTCTCTCCAGCGGAGCGCGCGGCGCTCAACCGCGCGCGCGCGCGCTCC 360

RESULT 13

US-10-741-600-17942

; Sequence 17942, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17942

; LENGTH: 58038

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-741-600-17942

Query Match 11.0%; Score 41.4; DB 8; Length 58038;

Best Local Similarity 49.8%; Pred. No. 0.032;

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Matches 132; Conservative 1; Mismatches 127; Indels 5; Gaps 1;
Qy 28 GGGCGCAACAGCAGCAGCGCGCGCGAGCTGGAGTTCGGGGTGGCGGGGA 87
Db 6432 GGACRCACGGGGCTTGGCGACGGCGGAGTGCCTCCAGGAGCGCGGCTTCGGGGCGGGG 6491
Qy 88 GGCAGCTGTCCGTGGTGTCTAGCGCCGCGAGCGCGCGGAGCGGCTGATCGGTCC 147
Db 6492 GCCGGGTGTCTTCCGCGGGCTCAGGGTGGAGCGGTGCACGGCTGTGTTCCG- 6550
Qy 148 CTCGAACATGGGAGGTTCAGTGGGTGCTTTAGGGCCCAAGCCCAACCGGCTCCAAA 207
Db 6551 ----ACCCCTCGCGCCCTCTGGCCCGCGCGGGCCCTTTACGGAGCCCTCCCA 6606
Qy 208 AGCTCCAGGCGCTCCCGAGCAGCGTGTCTCGGCCCTCTCTCGGTGAGAAAGTCGCC 267
Db 6607 AGACTCAAGGCTCGCGGGGCACTCGCTCTCCGCCCTTCCCGGAATCCAAACTTCCCTC 6666
Qy 268 CTGGGGGAGTTCGTCCCAAGGG 292
Db 6667 TGCAGCGCGCGCTTTCACGGAGGG 6691

RESULT 14
US-10-741-600-17681
; Sequence 17681, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17681
; LENGTH: 333811
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(333811)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17681

Query Match 11.0%; Score 41.4; DB 8; Length 333811;
Best Local Similarity 49.8%; Pred. No. 0.029;
Matches 132; Conservative 1; Mismatches 127; Indels 5; Gaps 1;
Qy 28 GGGCGCAACAGCAGCAGCGCGCGCGAGTGGAGTTCGGGGTGGCGGGGA 87
Db 191325 GGACRCACGGGGCTTGGCGACGGCGGCGAGTGCCTCCAGGAGCGCGGCTTCGGGGCGGGG 191384
Qy 88 GGCAGCTGTCCGTGGTGTCTAGCGCCGCGAGCGCGCGGAGCGGCTGATCGGTCC 147
Db 191385 GCCGGGTGTCCCTCCGCGGGCTCAGGGTGGAGCGGTGCAGCGGTGTGTTCCG- 191443
Qy 148 CTCGAACATGGGAGGTTCAGTGGGTGCTTTAGGGCCCAAGCCCAACCGGCTCCAAA 207
Db 191444 ----ACCCCTCGCGCCCTCTGGCCCGCGGGCCCTTTACGGAGCCCTCCCA 191499
Qy 208 AGCTCCAGGCGCTCCCGAGCAGCGTGTCTCGGCCCTCTCTCGGTGAGAAAGTCGCC 267
Db 191500 AGACTCAAGGCTCGCGGGGCACTCGCTCTCCGCCCTTCCCGGAATCCAAACTTCCCTC 191559
Qy 268 CTGGGGGAGTTCGTCCCAAGGG 292
Db 191560 TGCAGCGCGCGCTTTCACGGAGGG 191584

RESULT 15
US-10-017-161-1435
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; Sequence 1435, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABEURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1435
; LENGTH: 922
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(922)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(722)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(26)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (62)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (124)..(125)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (127)..(128)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (131)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (133)..(134)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (138)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (142)..(145)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (147)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (151)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (311)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (322)
; OTHER INFORMATION: a, t, c, g, unknown or other
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1	FEATURE:	
2	NAME/KEY: modified_base	
3	LOCATION: (326)	
4	OTHER INFORMATION: a, t, c, g, unknown or other	
5	FEATURE:	
6	NAME/KEY: modified_base	
7	LOCATION: (345)..(349)	
8	OTHER INFORMATION: a, t, c, g, unknown or other	
9	FEATURE:	
10	NAME/KEY: modified_base	
11	LOCATION: (351)..(361)	
12	OTHER INFORMATION: a, t, c, g, unknown or other	
13	FEATURE:	
14	NAME/KEY: modified_base	
15	LOCATION: (364)	
16	OTHER INFORMATION: a, t, c, g, unknown or other	
17	FEATURE:	
18	NAME/KEY: modified_base	
19	LOCATION: (366)..(368)	
20	OTHER INFORMATION: a, t, c, g, unknown or other	
21	FEATURE:	
22	NAME/KEY: modified_base	
23	LOCATION: (370)..(380)	
24	OTHER INFORMATION: a, t, c, g, unknown or other	
25	FEATURE:	
26	NAME/KEY: modified_base	
27	LOCATION: (384)	
28	OTHER INFORMATION: a, t, c, g, unknown or other	
29	FEATURE:	
30	NAME/KEY: modified_base	
31	LOCATION: (386)..(388)	
32	OTHER INFORMATION: a, t, c, g, unknown or other	
33	FEATURE:	
34	NAME/KEY: modified_base	
35	LOCATION: (392)	
36	OTHER INFORMATION: a, t, c, g, unknown or other	
37	FEATURE:	
38	NAME/KEY: modified_base	
39	LOCATION: (394)..(396)	
40	OTHER INFORMATION: a, t, c, g, unknown or other	
41	FEATURE:	
42	NAME/KEY: modified_base	
43	LOCATION: (403)	
44	OTHER INFORMATION: a, t, c, g, unknown or other	
45	FEATURE:	
46	NAME/KEY: modified_base	
47	LOCATION: (413)	
48	OTHER INFORMATION: a, t, c, g, unknown or other	
49	FEATURE:	
50	NAME/KEY: modified_base	
51	LOCATION: (415)..(417)	
52	OTHER INFORMATION: a, t, c, g, unknown or other	
53	FEATURE:	
54	NAME/KEY: modified_base	
55	LOCATION: (422)	
56	OTHER INFORMATION: a, t, c, g, unknown or other	
57	FEATURE:	
58	NAME/KEY: modified_base	
59	LOCATION: (438)..(439)	
60	OTHER INFORMATION: a, t, c, g, unknown or other	
61	FEATURE:	
62	NAME/KEY: modified_base	
63	LOCATION: (441)	
64	OTHER INFORMATION: a, t, c, g, unknown or other	
65	FEATURE:	
66	NAME/KEY: modified_base	
67	LOCATION: (443)	
68	OTHER INFORMATION: a, t, c, g, unknown or other	
69	FEATURE:	
70	NAME/KEY: modified_base	
71	LOCATION: (445)	
72	OTHER INFORMATION: a, t, c, g, unknown or other	
73	FEATURE:	

Job time : 430.232 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:25:32 ; Search time 101.11 Seconds
(without alignments)
1386.561 Million cell updates/sec

Title: US-09-977-579A-4_COPY_1_375

Perfect score: 375
Sequence: 1 cctcccttcgagtgagc.....gaagccgcagccccagaag 375

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	375	100.0	1261	6	US-10-374-954-8
C 2	44.8	11.9	169495	7	US-11-121-086-61
3	40.2	10.7	2838	6	US-10-770-726-27
C 4	39	10.4	1931	6	US-10-750-185-46989
C 5	37.8	10.1	160226	7	US-11-121-086-29
6	35.4	9.4	2793	6	US-10-750-185-32170
7	35.4	9.4	246960	7	US-11-121-086-8
C 8	35	9.3	5679	7	US-11-075-185-36
C 9	35	9.3	78869	7	US-11-075-185-1
10	34.8	9.3	1557	6	US-10-996-217A-6
11	34.8	9.3	2820	6	US-10-750-185-46988
C 12	34.8	9.3	161874	7	US-11-121-086-75
C 13	34.4	9.2	2375	7	US-11-108-528-63
14	34	9.1	1830	7	US-11-064-774A-120
C 15	33.8	9.0	150038	7	US-11-121-086-23
C 16	33.6	9.0	150468	7	US-11-112-908-56
C 17	33.6	9.0	193789	7	US-11-112-908-55
C 18	33.4	8.9	708	7	US-11-075-185-59
C 19	33.2	8.9	1386	6	US-10-509-464-3
20	33.2	8.9	5301	7	US-11-075-185-40
21	33.2	8.9	78869	7	US-11-075-185-1
C 22	33	8.8	191684	7	US-11-121-086-2
C 23	32.8	8.7	600	6	US-10-750-185-23

24	32.8	8.7	9710	6	US-10-655-872-1	Sequence 1, Appli
25	32.6	8.7	1975	6	US-10-750-185-56875	Sequence 56875, A
C 26	32.4	8.6	1777	6	US-10-750-185-60816	Sequence 60816, A
C 27	32.4	8.6	2786	7	US-10-750-185-29861	Sequence 29861, A
C 28	32.4	8.6	189252	7	US-11-121-086-54	Sequence 54, Appl
C 29	32.2	8.6	1434	7	US-11-075-185-57	Sequence 57, Appl
30	32.2	8.6	1723	7	US-11-051-568-28	Sequence 28, Appl
31	32.2	8.6	4854	6	US-10-821-234-103	Sequence 103, App
C 32	32.2	8.6	14172	7	US-11-075-185-2	Sequence 2, Appli
C 33	32.2	8.6	191091	7	US-11-121-086-60	Sequence 60, Appl
34	32	8.5	168516	7	US-11-121-086-3	Sequence 3, Appli
35	31.8	8.5	1196	6	US-10-750-185-47546	Sequence 47546, A
C 36	31.8	8.5	11070	7	US-11-075-185-34	Sequence 34, Appl
C 37	31.8	8.5	171162	7	US-11-112-908-38	Sequence 38, Appl
C 38	31.6	8.4	2276	6	US-10-131-826A-9	Sequence 9, Appli
C 39	31.6	8.4	180654	7	US-11-121-086-58	Sequence 58, Appl
C 40	31.6	8.4	235033	7	US-11-157-389-1	Sequence 1, Appli
C 41	31.6	8.4	237326	7	US-11-157-389-2	Sequence 2, Appli
C 42	31.4	8.4	168516	7	US-11-121-086-3	Sequence 3, Appli
C 43	31.4	8.4	171936	6	US-10-933-025-24	Sequence 24, Appl
C 44	31.4	8.4	172147	7	US-11-112-908-22	Sequence 22, Appl
C 45	31.4	8.4	188682	7	US-11-112-908-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8

Query Match 100.0%; Score 375; DB 6; Length 1261;

Best Local Similarity 100.0%; Pred. No. 8.5e-80;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CCCTCCCTTCGAGCTGAGCTTACCTGGCGGCGGAGGCGACGTGCTCCGTGGTGTCTGAGCGCCGCGGAGTGG	60
Db	1	CCCTCCCTTCGAGCTGAGCTTACCTGGCGGCGGAGGCGACGTGCTCCGTGGTGTCTGAGCGCCGCGGAGTGG	60
Qy	61	AAGCTGGAGTTCGCGGGTGGCGGAGGCGACGTGCTCCGTGGTGTCTGAGCGCCGCGGAGTGG	120
Db	61	AAGCTGGAGTTCGCGGGTGGCGGAGGCGACGTGCTCCGTGGTGTCTGAGCGCCGCGGAGTGG	120
Qy	121	GCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTTCGCTTAG	180
Db	121	GCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGGTTCGCTTAG	180
Qy	181	GGCCCAAGCCCCACCCCGGCTCAAAAGCTCCAGAGGCTCCCGAGGACCCGCTGCTCG	240
Db	181	GGCCCAAGCCCCACCCCGGCTCCAAAAGCTCCCGAGGCTCCCGAGGACCCGCTGCTCG	240

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Qy 241 GCCCTTCTTCGGTTCAGAAAGTCGCCCTGGGGGCGAGTTGTCCTCCAAAGGGTTTCTCTCG 300
Db 241 GCCCTTCTTCGGTTCAGAAAGTCGCCCTGGGGGCGAGTTGTCCTCCAAAGGGTTTCTCTCG 300
Qy 301 AAAGAAATCTGAGAGGGCGCAGTCTTACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAAATCTGAGAGGGCGCAGTCTTACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Qy 361 GCAGAGCCCCAGAG 375
Db 361 GCAGAGCCCCAGAG 375

RESULT 2
US-11-121-086-61/c
; Sequence 61, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-0000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 169495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (70072)..(70171)
; OTHER INFORMATION: a, c, g, t, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (139457)..(157244)
; OTHER INFORMATION: a, c, g, t, unknown or other
; US-11-121-086-61

Query Match 11.9%; Score 44.8; DB 7; Length 169495;
Best Local Similarity 56.7%; Pred. No. 0.02;
Matches 102; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy 74 GGGTGGCGGGGAGGCGACTGTCGTGTGTCAGCGCGCGGAGAGCGGGCGCGAGC 133
Db 45491 GGGAGGGCGGGTAGGGACCTTTACAGAGCCAGGAGGGCTTTTCGGGGCGGTGGGGCGCGC 45432
Qy 134 GCCTGATCGGTCCTCGAACTGGGGAGGTCAGTGGGTGCG-CTTAGGGCCAAAGCCC 192
Db 45431 TCGGAGCGGAGCGCGCGCTCGAGCGCGGTGCGTGGCGGCGAGTGTATGCAGACGGCGC 45372
Qy 193 CCACCGGCTCCAAAAGTCCCGAGGCGCTCCCGAGGACCGGTGCTCGGCGCTTCTCTCG 252
Db 45371 CGGCGCCGAAACCGAGCCCCGGGGGCTCCCGACCGCGGCTCCCGCGCTCCCGCG 45312

RESULT 3
US-10-770-726-27
; Sequence 27, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: CANCERS
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-27

Query Match 10.7%; Score 40.2; DB 6; Length 2838;
Best Local Similarity 49.8%; Pred. No. 0.25;
Matches 102; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 23 ACCCTGGGCGCAACGAGCGAGCGGGGCGCAGTGGAGCTGCGAGTTCCGGGGTGGGC 82
Db 577 ACCACGGCCAGAGGGGGCCCGAGGAAGGACGAGCGCGGTTCGCGCGTTCACAGC 636
Qy 83 GGGGAGGCGACTGTCGTGTGTCGTAGCGCGCGGCGAGCGGGCGCGGCGGCTGATCG 142
Db 637 GAGCGGTGCGCGCAGTGTGTGACGCGAGCGGGCGGGGCGAGAGAGAGCCCAAGTCT 696
Qy 143 GCTCCCTCGAACTGGGAGGTCCAGTGGGTGCGCTTAGGGCCCAAGCCCGCGCT 202
Db 697 TCCAGGGAGGGCTCAGGGGTCCCGAGGAGTCTCTCCCGGACAAACGCCCTCTCCGG 756
Qy 203 CAAAAGCTCCAGGGCTCTCCCGAG 227
Db 757 CCTGATGTCGGCACCCCGCGAGCCTG 781

RESULT 4
US-10-750-185-46989
; Sequence 46989, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46989
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-46989

Query Match 10.4%; Score 39; DB 6; Length 1931;
Best Local Similarity 52.8%; Pred. No. 0.48;
Matches 84; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 54 CGAGTGAAGCTGGAGTTCGGGGTGGCGGGGAGGCGACTGTCGTGTGCTGAGCGCC 113
Db 1745 CGAGAGGCGCTGGAGTCAACCACTTCATGGGGGCGACGCTGCCACCGCGCTGCA 1804
Qy 114 GCGAGAGCGGGCGGAGCGCTGATCGGCTCCCTCGAACTGGGAGGTCAGTGGGGT 173
Db 1805 AAGAGGAACAGGGTCAGAGCTGGAGATGGGATCACAGGGCGCCCTAGGTACAGTAGGCC 1864
Qy 174 CGCTTAGGGCCAAAGCGCCCGCGCTCCAAAGCTC 212
Db 1865 CTCTGAGACCTGGAGAGCGCTCCCGGCTTCATACCCCC 1903

RESULT 5
US-11-121-086-29/c
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; Sequence 29, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138-6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29
; LENGTH: 160226
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-29

Query Match          10.1%; Score 37.8; DB 7; Length 160226;
Best Local Similarity 52.2%; Pred. No. 0.86;
Matches 84; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Qy 49 GGGCGCAGTGAAGTCGAGTTCGGGGTGGGGGGGAGCGGAGTGTCCGTGTGCTGA 108
Db 141257 GGGCAGGCGGCGGGCGGGCGCGGAGGGGCGCGGAGCCGCCCAAGCGCGCGGA 141198

Qy 109 GCGCGCGGAGAGCGGCGCGGAGCGGTGATCGGCTCCCTCGAACTGGGAGGTCCAGT 168
Db 141197 GGGAGGCGGTGGAGCGGCTGGGGAGGAGGAGGAGTCTAGGGGAGGGGCGGCGAGG 141138

Qy 169 GGGGTGCTTAGGGCCCAAGCCCCACCGCGGCTCCAAAAG 209
Db 141137 CGGGGCGCGGGACCCCGCCCCCGCGCGGCTTTAAAG 141097

RESULT 6
US-10-750-185-32170
; Sequence 32170, Application US/10750185
; Publication No. US2005026603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750.185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32170
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Bovine 19866880392593
US-10-750-185-32170

Query Match          9.4%; Score 35.4; DB 6; Length 2793;
Best Local Similarity 51.6%; Pred. No. 3.3;
Matches 81; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 16 TGAGCTTACCTGGCGCAACGAGCGAGGCGGGCGCGAGTGGAGTGGAGTCCGG 75
Db 291 TGGGAGGAGCCCGCGGGGAGTGGGAGAGCTGTGTGAGGAGTGGAGGAGCGCGGAG 350

Qy 76 GGTGGCGGGAGGCGGAGTGTCCGTGTGAGCGCGGCGGAGAGCGGGCGCGGAGCGG 135
Db 351 GGAGTGGGAGGAGCGCGCGGGGGAATGGGAAGGAAACCGCGGAGGAGTGGGAGGCC 410
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Qy 136 CTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGGGG 172
Db 411 GCGGGGAGTGGGAGGAGCTGCTGAGGACAGGAGG 447

RESULT 7
US-11-121-086-8
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138-6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-8

Query Match          9.4%; Score 35.4; DB 7; Length 246960;
Best Local Similarity 49.7%; Pred. No. 3.1;
Matches 90; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Qy 74 GGGTGGGCGGGAGGCGACTGTCCGTGTGTGAGCGCGCGGAGAGCGCGGCGGAGC 133
Db 152668 GGGTCCGGGTACAGCCCCCGGCGCGCGCGCGCGCGCGCGCGCGCGCTCC 152727

Qy 134 GGCTGATCGGCTCCTCGAACTGGGAGGTCCAGTGGGGTGGCTTAGGGCCCAAGCCCC 193
Db 152728 GGCGCGCTGGCTCCGGCGCGCGGTGTGTCAGCGGCCCGCGGCTCCGGGGCATGTCCAG 152787

Qy 194 CACCGCGCTCCAAAAGCTCCAGGCGCTCCCGAGGACCCCGTGTCTCGGGCCCTTCTTCGG 253
Db 152788 CCACTGGCTCCGCGCGCGCGCGCTCCCGGGCTCCCGGGCTCCCTTGGCTGCCGGAGCCTCGC 152847

Qy 254 T 254
Db 152848 T 152848
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```
RESULT 8
US-11-075-185-36/c
; Sequence 36, Application US/11075185
; Publication No. US2005026643A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075.185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
; LENGTH: 5679
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-36

Query Match          9.3%; Score 35; DB 7; Length 5679;
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Best Local Similarity 46.8%; Pred. No. 4.1;
Matches 110; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
Qy 89 GCGACTGTCGTGTGTAGCGCGCGGAGAGCGGCGGAGCGGTGATCGGCTCCC 148
Db 4036 GCGTCACACAGAGCTCGGTCCGCCGACGTCGCGGCGGAGAGCCACCCCTGCACCA 3977
Qy 149 TCGAACCTGGGAGTCCAGTGGGTGCTTAGGGCCCAAGAGCCGCCCGGCTCCAAAA 208
Db 3976 GGGCCAGCGCCCGGACCGCGGCTGCACGGCGCGGAGACCGCGCTGTCATCGCCCG 3917
Qy 209 GCTCCAGGCGCTCCCGAGCACCGGTGCTCGGCCCTTCCTTCGGTCAGAAAGTCGCCCC 268
Db 3916 CCGTCAGTCCACAGCACCGCGCGCGCGCGCGCGCTCCGCCAGCGCTCGAGCA 3857
Qy 269 CTGGGGGAGTTCCTCCAAAGGTTTCTCGAAAGAAATCTGAGAGGCGGAGTTC 323
Db 3856 GCTCCGCGAGCGCGCGCGCGCGCGACGCCAGCGCGCGCGCGAGCGCACCGCTC 3802

RESULT 9

US-11-075-185-1/c
; Sequence 1, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 78869
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1

Query Match 9.3%; Score 35; DB 7; Length 78869;
Best Local Similarity 46.8%; Pred. No. 3.9;
Matches 110; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
Qy 89 GCGACTGTCGTGTGTAGCGCGCGGAGAGCGGCGGAGCGGTGATCGGCTCCC 148
Db 30267 GCGTCACACAGAGCTCCGTGCGCGCCAGCTGCGGCGCGGAGGACACCCCTGCACCA 30208
Qy 149 TCGAACCTGGGAGTCCAGTGGGTGCTTAGGGCCCAAGAGCCGCCCGGCTCCAAAA 208
Db 30207 GGGCCAGCGCGCGGACCGCGGCTGCACGGCGCGAGCACCGCGCTGATCGCCCG 30148
Qy 209 GCTCCAGGCGCTCCCGAGCACCGGTGCTCGGCCCTTCCTTCGGTCAGAAAGTCGCCCC 268
Db 30147 CCGTCAGTCCACAGCACCGCGCGCGCGCGCGCGCGCTCCGCCAGCGCTCGAGCA 30088
Qy 269 CTGGGGGAGTTCGTCCTCCAAAGGTTTCTCGAAAGAAATCTGAGAGGCGGAGTTC 323
Db 30087 GCTCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCGCACCGTTC 30033

RESULT 10

US-10-996-217A-6
; Sequence 6, Application US/10996217A
; Publication No. US20050266561A1
; GENERAL INFORMATION:
; APPLICANT: Revivicor, Inc.
; APPLICANT: Wells, Kevin
; TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals

FILE REFERENCE: 10785.105070 REV 1015 US
CURRENT APPLICATION NUMBER: US/10/996,217A
CURRENT FILING DATE: 2004-11-22
PRIOR APPLICATION NUMBER: 60/523,938
PRIOR FILING DATE: 2003-11-21
NUMBER OF SEQ ID NOS: 272
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 1557
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-996-217A-6

Query Match 9.3%; Score 34.8; DB 6; Length 1557;
Best Local Similarity 48.9%; Pred. No. 4.6;
Matches 93; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
Qy 28 GGGCGCAACGAGCGAGGCGGCGCGAGTGGAAAGCTGGAGTTCCCGGGGTGGCGGGGA 87
Db 1329 GG 1388
Qy 88 GGGCACTGTCGTGTGCTGAGCGCCCGGCGAGAGCGGCGCGAGCGGCTGATCGGCTCC 147
Db 1389 GG 1448
Qy 148 CTGCAACTGGGAGGTCCAGTGGGTGCTTAGGGCCCAAGCCCCCAGCGGCTCCAAA 207
Db 1449 GG 1508
Qy 208 AGCTCCCCAGG 217
Db 1509 CTGCCCCAAG 1518

RESULT 11

US-10-750-185-46988
; Sequence 46988, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46988
; LENGTH: 2820
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-46988

Query Match 9.3%; Score 34.8; DB 6; Length 2820;
Best Local Similarity 53.7%; Pred. No. 4.6;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
Qy 111 GCCGCGAGAGCGGCGGCGGAGCGGTGATCGGCTCCCTCGAACTGGGAGGTCCAGTGG 170
Db 1413 GCTGAGGAGACACAGGCGGAGCTGCTGAAGCCATCCCTGACCTAGACTGTGCGAGCAA 1472
Qy 171 GGTCTTAGGGCCCAAGCCCCCAGCGGTCCAAAAGTCCCAAGGCTCCCGAGGCTCCCGCAGCA 230
Db 1473 GGCCACCCAGCGGAGCGGCGGCGGAGCCCGGAGCACAAAACCCCGGAGACACCCCGGCGC 1532

```
Qy 231 CCGGTGTCGGCCCC 244
Db 1533 CAGAAGGCAGCCCC 1546

RESULT 12
US-11-121-086-75/c
; Sequence 75, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 161874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-75

Query Match 9.3%; Score 34.8; DB 7; Length 161874;
Best Local Similarity 60.6%; Pred. No. 4.3;
Matches 57; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 45 GCAGGGCGCGAGTGGAGCTGGAGTTCGGGGTGGCGGGAGGCGACTGTCGTGGTG 104
Db 77243 GCGGGGCGGGGTGGGAACCTCGGAAACCTCGGAGGCGGGAGCGGCTGCAAGGGGCG 77184

Qy 105 CTGAGCGCCGCGAGAGCGGCGGAGCGGCTG 138
Db 77183 GGGAGGCGGAGCCCGCAGCGGAGGGGCGG 77150

RESULT 13
US-11-108-528-63
; Sequence 63, Application US/11108528
; Publication No. US20050261189A1
; GENERAL INFORMATION:
; APPLICANT: Larsen, Glenn
; APPLICANT: Marvin, Martha
; APPLICANT: Li, Dean Y.
; APPLICANT: Wang, Elizabeth
; APPLICANT: Chen, C. M. Amy
; APPLICANT: Shamah, Steven M.
; TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
; FILE REFERENCE: HDR-P01-041
; CURRENT APPLICATION NUMBER: US/11/108.528
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,137
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/598,368
; PRIOR FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 2375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-108-528-63

Query Match 9.2%; Score 34.4; DB 7; Length 2375;
Best Local Similarity 45.5%; Pred. No. 5.7;
Matches 122; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

Qy 88 GCGGACTGTCGTGCTGAGCGCGGAGAGCGGGCGGAGCGGCTGATCGGCTCC 147
```

```
Db 274 GCGGGTCCCGGGGGTGTCTGCCCATGAGCGGGAGCGCGGCTGTCTCTCCGGAG 333
Qy 148 CTGAACTGGGGAGGTCCAGTGGGGTCCAGTGGGGCCAAAGCCCCACCCCGGTCCAAA 207
Db 334 CCTGACCCGAGTCGGAGCTGTGTGTCGAGCGCCCGCCCGCCGATCATGCGCC 393
Qy 208 AGTCCAGGGCTCCCGACGACCGGTGTGCGGCCCTTCTTCGTGAGTGAAGTCTGCC 267
Db 394 GGGGCCCTGGCTCTCCAGTCCCACTGGGTGTGAGCCCCCACTCCAGCCGCTCAGG 453
Qy 268 CTTGGGGGAGTTCGTCCCAAGGGTTTCTCGAAAGAACTGAGAGGGCGCAGTCTCT 327
Db 454 CTTGCGCGCATGGGACGCGCCACCTCGCCCTGTGCGGTCTCCAGCCAGCCCCA 513
Qy 328 ACCAGGGAATCTCTCTGTGTAGCCTTG 355
Db 514 GCGGGCCAGCGCTCTGGGTGCTCCTG 541

RESULT 14
US-11-064-774A-120
; Sequence 120, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH
; FILE REFERENCE: 28967/35977B2
; CURRENT APPLICATION NUMBER: US/11/064.774A
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 120
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Orf virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (312)..(755)
US-11-064-774A-120

Query Match 9.1%; Score 34; DB 7; Length 1830;
Best Local Similarity 51.3%; Pred. No. 7.1;
Matches 79; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 40 GCGAGCGGGCGCGAGTGGAGCTGAGTTCGGGGTGGCGGGAGGCGACTGTCCG 99
Db 1565 GCGGCGCGCGGGCGCTCGCGCGGGGCTGTCTGCGCGGGCGGGCGCGCGGCG 1624
Qy 100 TGTGCTGAGCGCGCGAGAGCGGGCGCGAGCGGCTGATCGGCTCCCTCGAACTCGGG 159
Db 1625 GGCTGGCGCGCGCTGCGGCGCGGGCGCGGGGGTAGCGCGCCCGCCCGCGGCG 1684
Qy 160 AGGTCCAGTGGGGTCTGTTAGGGCCCAAGCCCC 193
Db 1685 CCGCGCGCAGCCCTTGCCCGGACCGAGCGCCAC 1718

RESULT 15
US-11-121-086-23/c
; Sequence 23, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
```

; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 150038
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-23

Query Match 9.0%; Score 33.8; DB 7; Length 150038;
Best Local Similarity 54.4%; Pred. No. 7.4; Indels 0; Gaps 0;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 48 GGGGCGCGAGTGGAGCTTCCGGGGTGGCGGGGAGCGACTGTCGGTGGTCTG 107
Db 26692 GTGGTGGAGGTGGCGGGTGGAGATGGCGGGTGGAGGTGGGTGGAGATGGCG 26633

Qy 108 AGCGCGCGGAGAGCGGGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCCAG 167
Db 26632 GGTGGTGGAGGTGGCGGGTGGCGGGTGGCAGAGGTGGTGGAGGTGGTGGAGG 26573

Qy 168 TGGGG 172
Db 26572 TGGCG 26568

Search completed: December 13, 2005, 14:42:57
Job time : 106.11 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	143.8	22.2	617	3	US-09-949-016-2369	Sequence 2369, Ap	
2	51	7.9	11174	3	US-09-949-016-14111	Sequence 14111, A	
3	48.6	7.5	30337	3	US-09-949-016-13053	Sequence 13053, A	
4	45.4	7.0	1645	3	US-09-023-587A-5	Sequence 5, Appl	
5	44.8	6.9	1053	3	US-09-902-540-2666	Sequence 2666, Ap	
C 6	44.8	6.9	13706	3	US-09-902-540-1124	Sequence 1124, Ap	
C 7	42.4	6.5	2133	3	US-09-902-540-4106	Sequence 4106, Ap	
8	42.4	6.5	23738	3	US-09-902-540-1203	Sequence 1203, Ap	
9	41.6	6.4	636	3	US-09-489-035A-3591	Sequence 3591, Ap	
10	40.6	6.3	2943	3	US-09-902-540-3929	Sequence 3929, Ap	
11	40.6	6.3	21295	3	US-09-902-540-1194	Sequence 1194, Ap	
12	40.4	6.2	1533	3	US-09-902-540-7877	Sequence 7877, Ap	
13	40.4	6.2	5228	3	US-09-902-540-789	Sequence 789, App	
14	39.2	6.0	732	3	US-09-902-540-3806	Sequence 3806, Ap	
15	39.2	6.0	6202	3	US-09-774-528-120	Sequence 120, App	
16	39.2	6.0	6202	3	US-10-120-988-120	Sequence 120, App	
C 17	39.2	6.0	18551	3	US-09-902-540-1187	Sequence 1187, Ap	
18	38.6	6.0	513	3	US-09-902-540-8812	Sequence 8812, Ap	
19	38.6	6.0	1407	3	US-09-902-540-6215	Sequence 6215, Ap	
20	38.6	6.0	8122	3	US-09-902-540-937	Sequence 937, App	
21	38.6	6.0	13332	3	US-09-902-540-1047	Sequence 1047, Ap	
22	38.2	5.9	1437	3	US-09-902-540-8578	Sequence 8578, Ap	
23	38.2	5.9	9081	3	US-09-902-540-905	Sequence 905, App	
24	38	5.9	2692	3	US-10-104-047-1554	Sequence 1554, Ap	

Db 251 CACCAAGACCTGCAGGATCTGTCTATCTTCATCACCAATGCTACCAACCACTCGG 310
Qy 348 CCTCTACACCTGCATGTCCGGAGTTTGAGTTTGAGGGCATCGCCCTTTGTCAA 407
Db 311 CGACTACAGGTGCCACGCTTACCGCTCTTCTTCGAAAACCTACGAGCACACACAG 370
Qy 408 GACGACGGGCTGATCCCTTAAGAGTCCACGAGGAGCTGGAGAGGACTTCACCTCTGT 467
Db 371 CGTCGTCAGAAGATCCACATAGGTAGTGACAAAGCCACAGACATGGCATCAT 430
Qy 468 GGTCTCAGAAATCATGATCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 527
Db 431 CGTGTCTGAGATCATGATGTGTCTCATTTGTGTGTGTGTGTGTGTGTGTGTGTGT 490
Qy 528 GATGATATTTGCTACAGAAAGGTTCTCAAAAGCCGAAGAG---CGAGCCCAAGAAACGC 584
Db 491 GATGATTTTACTGCTACAAAGAGATCGCTGCGCCACCGGAGACTGCTGCACAGGAATGC 550
Qy 585 GTCTGACTACCTTGCCATCCCATCTTGAGAACAAAGGAGAACTCTGCGG 631
Db 551 CTCGGAATACCTGGCCATCACCTCTGAAGCAAGAGAACTGCACGG 597

RESULT 2

US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111

Query Match 7.9%; Score 51; DB 3; Length 11174;
Best Local Similarity 58.1%; Pred. No. 0.001;
Matches 90; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 66 CTTCCCTGTGTGTGGAAGTCCCTCGAGACGGAGCCGTGACGGCAACCCCATGAA 125
Db 2011 CTCGGGGGCTGCGTGGAGGTGGACTCGGAGACCGAGCCGTGTATGGGATGACCTTCAA 2070
Qy 126 GCTGGCTGTCATCTCCTCATGAAGAGAGAGGTGGAGGCCACACCGTGGTGAATG 185
Db 2071 AATCTTTGATCTCTCTCAAGCCGCGGAGGAGACCAACCGTGNAGACTTCACCGAGTG 2130
Qy 186 GTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTA 220
Db 2131 GACCTTCGCCCAAGAGGGCACTGAGGAGTTTGTCA 2165

RESULT 3

US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13053
; LENGTH: 30337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(30337)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053

Query Match 7.5%; Score 48.6; DB 3; Length 30337;
Best Local Similarity 63.0%; Pred. No. 0.0068;
Matches 75; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 454 GACTTCACCTCTGTGGTCTCAGAAATCATGATGTACATCTTCTGTGTTCTTCTCACCTG 513
Db 620 GACATGCCATCCATCGTGTCTGAGATCATGATGTATGTCTATTGTGTTGTTGACCAT 679
Qy 514 TGGCTGCTCATCGAGATGATATTTCTACAGAAAGTCTCAAAAGCCGAGAGGCAGC 572
Db 680 TGGCTGTCGAGAGATGATTACTGTCTACAAGAGATCGTCTGCCGCCACCGAGACTGC 738

RESULT 4

US-09-023-587A-5
; Sequence 5, Application US/09023587A
; Patent No. 6653530
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, Christine K.
; APPLICANT: Bhat, Ganesh B.
; APPLICANT: Venkatramesh, Mylavaram
; APPLICANT: Rangwala, Shaikat H.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Boddupalli, Sekhar S.
; TITLE OF INVENTION: Methods for Producing Carotenoid Compounds, Tocopherol Compounds,
; SPECIALTY OILS IN PLANT SEEDS
; FILE REFERENCE: 16516.122
; CURRENT APPLICATION NUMBER: US/09/023,587A
; CURRENT FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1645
; TYPE: DNA
; ORGANISM: Zea mays
US-09-023-587A-5

Query Match 7.0%; Score 45.4; DB 3; Length 1645;
Best Local Similarity 46.2%; Pred. No. 0.018;
Matches 151; Conservative 0; Mismatches 176; Indels 0; Gaps 0;
Qy 54 GGTCAAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACGGAGCCGTCAGGG 113
Db 349 GGTGTCACCGCTCTTCTTAAGGTACGAGCGCCCAAGAGCCGACGCTGTAGCT 408
Qy 114 CAACCCCATGAAGTGGCGTGCATCTCTCATGAAGAGAGAGAGGTGGAGGCCACAC 173
Db 409 GGTGCACTACCAACCACTACGACGCGCAGCAACGGCAAGTCTCGCGCGGAGAGCGTCT 468

174	Qy	GGTGGTGGAAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCTTATTATACGAGTATCG	233
469	Db	CGAGGTGGACGCGATCGTGGCGCGGGA CGGCGCCAACTCTCGCGTGGCAACGACATGGG	528
234	Qy	GAATGGCCACACAGAGGTGGAGAGCCCTTTTCAGGGCGCTGCAGTGGAAATGGCAGCAA	293
529	Db	CGCGGGCGACTACAGGATCGCCATCGCGTTTCAGGAGCGGTTCAAGATCCCGCAGCAA	588
294	Qy	GGACCTGCAGGACGCTGTCATCATCTGTGCTCAA CGTCACTCTGAACGACTCTGGGCTCTTA	353
589	Db	GATGGTGTACTACGAGGAGCGCGGAGATGACGTCGGCGACGACGCTCTCTCCCGACTT	648
354	Qy	CACCTGCAATGTGTCCCGGAGTTTGA	380
649	Db	CTACGGCTGGGTGTTTCCCAAGTGGCA	675

RESULT 5

```

US-09-902-540-2666
; Sequence 2666, Application US/09902540
; Patent NO. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2666
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2666

```

Query Match	6.9%;	Score 44.8;	DB 3;	Length 1053;
Best Local Similarity	52.1%;	Pred. No. 0.022;		
Matches 100;	Conservative 0;	Mismatches 92;	Indels 0;	Gaps 0;
Qy	61	GTCTGCTTCCTGTGTGTGTGGAAGTGCCTCCGAGACGGAGGCCGTGCAGGCGAACCC	120	
Db	151	GACTTCTCCAGGACTGGTGGACTGGCTCGAAGATGACGGACGGAGCGCCACTC	210	
Qy	121	ATGAAGTGGCCTGCATCTCTTGTCATGAAGAGAGAGGAGGTGAGGCCACCACGGTGGTG	180	
Db	211	ATCCACCGGCTGGTGGGGCTTCTTCGCACGGGTGACAGCATCTGTCGGCACCAACCTGGT	270	
Qy	181	GAATGGTTCTACAGGCCCGGGGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC	240	
Db	271	CTGAACTCTACAGACCTGAACGCCCTGAGGGCGGATGTACTGTTCGGCGCAGCTC	330	
Qy	241	CACCAGGAGGTG	252	
Db	331	TACGAGGAGCG	342	

RESULT 6

```

RES001 6
US-09-902-540-1124/C
; Sequence 1124, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902.540

```

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; CURRENT FILING DATE: 2001-07-10
;
; PRIOR APPLICATION NUMBER: 60/217,883
;
; PRIOR FILING DATE: 2000-07-10
;
; NUMBER OF SEQ ID NOS: 16825
;
; SEQ ID NO 1124
;
; LENGTH: 13706
;
; TYPE: DNA
;
; ORGANISM: Myxococcus xanthus
;
US-09-902-540-1124

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Query Match	6.9%	Score 44.8;	DB 3;	Length 13706;
Best Local Similarity	52.1%;	Pred. No. 0.056;		
Matches 100;	Conservative 0;	Mismatches 92;	Indels 0;	Gaps 0;
Qy	61	GTCTGCTTCCTGTGTGTGGGAAGTCCCTCGAGACGGAGGCGCTGCGAGGGCAACCCC	120	
Db	4948	GACTTCTTCACGGACCTGGTGGACCTCGCGCTCGAAGATGACGGACGGAGCGCCACCTC	4889	
Qy	121	ATGAAGTGGCGCTGCATCTCCTCGATGAAGAGAGAGGAGGTGAGGCGCACACCGGTGGTG	180	
Db	4888	ATCCACCGGTGGTGGCGTCTTCCTCGACGGGTGACAGCATCGTTCGGGCACAAACCTCGGTG	4829	
Qy	181	GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCTCTATTATTCAGAGTATCGGAATGGC	240	
Db	4828	CTGAACCTCTACAGACCTGAACGCCCTTGAGGGCGGGATGTACCTGTTCGCCCCAGCTC	4769	
Qy	241	CACAGGAGGTG	252	
Db	4768	TACGAGGAGGCG	4757	

RESULT 7

```

US-09-902-540-4106/c
: Sequence 4106, Application US/09902540
: Patent No. 6833447
:
: GENERAL INFORMATION:
:
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Wiegand, Roger C.
:
: TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
:
: FILE REFERENCE: 38-10(15849)B
:
: CURRENT APPLICATION NUMBER: US/09/902,540
:
: CURRENT FILING DATE: 2001-07-10
:
: PRIOR APPLICATION NUMBER: 60/217,883
:
: PRIOR FILING DATE: 2000-07-10
:
: NUMBER OF SEQ ID NOS: 16825
:
: SEQ ID NO 4106
:
: LENGTH: 2133
:
: TYPE: DNA
:
: ORGANISM: Myxococcus xanthus
:
US-09-902-540-4106

```

Query Match	6.5%;	Score 42.4;	DB 3;	Length 2133;
Best Local Similarity	51.6%;	Pred. No. 0.13;		
Matches 97;	Conservative 0;	Mismatches 91;	Indels 0;	Gaps 0;
Qy	87	GCCCTCGAGACGAGGCGGTGCGAGGCAACCCCATGAAGCTGGCGTGCATCTCTCGAT	146	
Db	1813	GGCCAGGATGATGCGGCGCGCCATCCCGTTCGAAGACGCGTGCAGCGGCGTGCAG	1754	
Qy	147	GAAGAGAGAGAGGTGGAGGCGCCACCGTGGTGGGATGGTTCTACAGGCGCCGAGGGCGG	206	
Db	1753	GAACGGGCGCGGAGTCGACACGCTGGCGGTGGGACCGCTTCCACGACCACTGTCGT	1694	
Qy	207	TAAAGATTTCTTTATTTTACGAGTATCGGAATGCGCACCGAGGTGAGAGCCCCCTTTCA	266	
Db	1693	GGGTGAAGCGTCCGCTACGAGGATCTGCGGGACTCCAGCTCGGACAGCGCGCGTGCA	1634	
Qy	267	GGGGCGCC	274	
Db	1633	GCTCCGCC	1626	

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RESULT 8
US-09-902-540-1203
; Sequence 1203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1203
; LENGTH: 23738
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1203

Query Match          6.5%; Score 42.4; DB 3; Length 23738;
Best Local Similarity 51.6%; Pred. No. 0.31;
Matches 97; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 87 GCCCTCGAGACGAGGCGCGTGCAGGGCAACCCCATGAGCTGCGCTGCATCTCTCGAT 146
DB 4191 GCGCAGGATGATGGCGGCGGCCATCCGTTTCAAGACGCGGTGCAAGCCGCGTGCAG 4250
QY 147 GAAGAGAGAGGAGTGGAGGCCACACACGCTGGTGGATGTTCTACAGGCCGAGGGCGG 206
DB 4251 GAAGCGGCGCGGAGTGGACACGCTGGCGTGGGACCGCTTCCGACCACTGCTGT 4310
QY 207 TAAAGATTTCCTATTATACGAGTATCGGAATGGCCACACGAGGAGTGGAGAGCCCTTTCA 266
DB 4311 GGGTGAACGCTCCGCTACGAGGATCTGCGCGGACTCCAGCTCGACAGCGCGGTGCA 4370
QY 267 GGGCGGCC 274
DB 4371 GCTCGGCC 4378

RESULT 9
US-09-489-039A-3591
; Sequence 3591, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3591
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3591

Query Match          6.4%; Score 41.6; DB 3; Length 696;
Best Local Similarity 48.3%; Pred. No. 0.14;
Matches 116; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 83 AAGTCCCTCGAGACGAGGCGCGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTCT 142
DB 92 AGGCGCGGACGCTCGCGCAGCGCGTGTGGCAAGCTGCCGAAGCGCGGCTATGCCGACT 151
QY 143 GCATGAAGAGAGAGGAGTGGAGGCCACACGCTGTGTAATGTTCTACAGGCCCGGAGG 202

Db 152 ACCTGCGGTTCAACGACGTTTGACGGTACCCCGCTGGATCAGGGGATTCGCTGTGGTTCC 211
QY 203 GCGGTAAGATTTCTTATTTACGAGTATCGGAATGCCACACGAGGAGTGGAGAGCCCT 262
DB 212 CCGGGCCGAATCTCTTTTACCGGGGAAGATGTGCTTGAGCTGACAGGGCCACGCGGCCCCGG 271
QY 263 TTCAGGGGCGCTCGAGTGGGAATGGCAGCAAGGACCTGCAGGAGCTGTCCATCACTGTGC 322
DB 272 TCATTCTGACCTGCTGCTTAAACGATATTCTGACCCCTGCCGGGCTGGGATGCCAGGC 331

RESULT 10
US-09-902-540-3929
; Sequence 3929, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3929
; LENGTH: 2943
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3929

Query Match          6.3%; Score 40.6; DB 3; Length 2943;
Best Local Similarity 48.9%; Pred. No. 0.45;
Matches 109; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 85 GTGCGCTCGAGAGGAGCGCGTGCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGC 144
DB 1831 GTGCTGGAAGAGGTGGAGCGCGCGCTGCGGAGTGTGCGCTGATGCCGCGAGGCCGCG 1890
QY 145 ATGAAGAGAGAGGAGGTGGAGGCCACCAACGCTGTGGAATGTTCTACAGCCCGAGGCG 204
DB 1891 ATGCGCTACGCGCAGAGAGCTGAAGCCCGCGGTGAGCGCGCGCGCCAGGTGAAGGC 1950
QY 205 GGTAAAGATTTCTTATTTACGAGTATCGGAATGGCCACACGAGGAGTGGAGAGCCCTTT 264
DB 1951 GCCTATGACCGCTCTCTGGACGTGCGCAGCTTCACCGCGCGCGTGGAGCGCTGTGTG 2010
QY 265 CAGGGGCGCTGCACTGGATGGCAAGGACCTGCAGGACG 307
DB 2011 AAGCGCGCCAGGAGCGCATGGGCGATCAGGCGCAGAGGAGG 2053

RESULT 11
US-09-902-540-1194
; Sequence 1194, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1194
; LENGTH: 21295
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; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1194

Query Match          6.3%; Score 40.6; DB 3; Length 21295;
Best Local Similarity 48.9%; Pred. No. 0.94; Indels 0; Gaps 0;
Matches 109; Conservative 0; Mismatches 114;

Qy 85 GTGCCCTCGGAGACGGAGCGCGTGCAGGGCAACCCCATGAAGCTGCGGTGCATCTCTGTC 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2609 GTGCTGGAAGAGGTGGAGGCGCGCTGCGCAGCTGCGCTGATGCCGCGGAGGCGCGC 2668

Qy 145 ATGAAGAGAGAGGAGGTGGAGGCCACACGCGTGTGTGAATGTTCTACAGGCCCGAGGGC 204
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2669 ATGGCCTACGCGCAGGAGCTGAAGGCCCGCGCTGGAGGCGCGCGCCAGGTGAAGCGC 2728

Qy 205 GGTAAAGATTTCCTATTATTACAGTATCGGAATGCCACACAGGAGGTGGAGGCCCTTT 264
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2729 GCCTATGACCCTGCTTGGACGTGCGCAGCTTCGACCGGCCCGCGGTGGAGCGCTGGTG 2788

Qy 265 CAGGGGCGCCTGCAGTGAATGGCAGCAAGGACCTGCAGGACG 307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2789 AAGCGGCCCAAGGAGCGCATCGAGGCCACGAGGAGG 2831

RESULT 12
US-09-902-540-7877
; Sequence 7877, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 7877
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-7877

Query Match          6.2%; Score 40.4; DB 3; Length 1533;
Best Local Similarity 47.9%; Pred. No. 0.4;
Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 232 CGGAATGCCACCGAGGAGGTGGAGAGCCCTTTTCAGGGGCGCCTGCAGTGAATGGCAGC 291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 CGGGATGCCCGAGCAGTTGAGTCTCCGAGGGAGGGCTCGTCTCGGGATGGGGAC 369

Qy 292 AAGGACCTGCAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCTC 351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 ACGGAGCTGCAGGACCTGTGTGGCGCGGTACAGGTGACGGCGGGCTGCTCAGTGGGC 429

Qy 352 TACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAAGGCGCATCGGCCCTTTTGTGAAGACG 411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 TTCAGCAGCAGCCATCGCGTGGGCTCGTGAAGGGGGCGCTGGCGAAGGTGGGCATCACC 489

Qy 412 ACGGGCTGATCCCTTAAGAGTCAACGAGAGGCTTGAGAGGACTTCACCTCTGTGGTC 471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 490 GTGCTGGTCGCGCTGCTGCTTTCACCGCGCGGCGCTTCTGGTCAAGCGCCATCGTG 549

Qy 472 TC 473
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Db 550 TC 551

RESULT 13
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US-09-902-540-789
; Sequence 789, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 789
; LENGTH: 5228
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-789

Query Match          6.2%; Score 40.4; DB 3; Length 5228;
Best Local Similarity 47.9%; Pred. No. 0.64;
Matches 116; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 232 CGGAATGCCACCGAGGAGGTGGAGAGCCCTTTTCAGGGGCGCCTGCAGTGAATGGCAGC 291
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3057 CGGGATGCCCGAGCAGTTGAGTCTCCGAGGGAGGGCTCGTCTCGGGATGGGGAC 3116

Qy 292 AAGGACCTGCAGGAGCTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCTC 351
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3117 ACGGAGCTGCAGGACCTGTGGCGCGGTACCAAGGTACGCCGCTGGTCCACGTGGGC 3176

Qy 352 TACACCTGCAATGTGTCCCGGAGTTTGAAGTTCAGGCGCATCGGCCCTTTGTGAAGACG 411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3177 TTCAGCGCACCCATGCGGTGGCTGCTGGAAGGGGCGCTGGCGAAGCTGGGCATCACC 3236

Qy 412 ACGCGGCTGATCCCTTAAGAGTCAACGAGAGGCTTGAGAGGACTTCACCTCTGTGGTC 471
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3237 GTGCTGGTCGCGTCTGCTTTCACCGCGCGGCGCTTCTGCTGTGTCAGCGCGGCATCGTG 3296

Qy 472 TC 473
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Db 3297 TC 3298

RESULT 14
US-09-902-540-3806
; Sequence 3806, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3806
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3806

Query Match          6.0%; Score 39.2; DB 3; Length 732;
Best Local Similarity 49.5%; Pred. No. 0.66;
Matches 101; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy 297 CCTGAGGAGCGTGTCCATCACTGTGCTCAACGTCACCTCTGAACGACTCTGGCTCTACAC 356
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Db      480  CCTGAGGACATGTCGGACGACGTGAAGATCGCGCGCTCAAGGCGCTGGGCGTCTTCAA 539
Qy      357  CTGCAATGTGTCGCGGAGTTTGAGTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCG 416
Db      540  GTACGAGCGCGCGCGGAGCCCATGCTGAAGCTCTCACCGCCGACGAGACGGCTCGCGG 599
Qy      417  GCTGATCCCCCTAAGAGTCACGAGGAGGCTGGAGAGACTTTCACCTCTGTGGTCTCAGA 476
Db      600  GGTGACAGCTCCGCTACTCAGCGCGCTGCGGAAAGGTGGCTTCTCCGTGAGGGCTACCG 659
Qy      477  AATCATGATGTACATCCTTCTTGGT 500
Db      660  GGAGAGGTGGAGCGCGTGTGTTGT 683
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RESULT 15
US-09-774-528-120
; Sequence 120, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 120
; LENGTH: 6202
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)...(4890)
US-09-774-528-120
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Query Match      6.0%; Score 39.2; DB 3; Length 6202;
Best Local Similarity 47.2%; Pred. No. 1.4;
Matches 119; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

Qy      93  GGAGACGAGCGCGTGACGGCAACCCCATGAAGCTGCGTGCATCTCTCGATGAAGAG 152
Db      2418 GCACAAGGAGTCTGGGGAGAGCACGGTGACATGCTGAAGCGCAAGGCGGAGTGGAGA 2477
Qy      153  AGAGAGGTGGAGGCCACACCGTGTGGTGAATGTTTACAGGCCCGGAGGGCGGTAAAGA 212
Db      2478 GCGGAGGAAGGTTTGTACCACCTGACGAGAGGCGCTGCAGCAGGAGCAGAGACAACGC 2537
Qy      213  TTTCCTTATTACAGATATCGGAATGCGCAACAGAGGTGGAGAGCCCTTTTCAGGGCGG 272
Db      2538 CCTGCCATGGCGAGAACCAAGAGGCTGCGGGCGAGCTGGACAGGGTCAATTTCTCTGCA 2597
Qy      273  CTGCAGTGGATGCGACGACGAGGACCTGCAGAGCTGTCCATCACTGTGCTCAACGTCAC 332
Db      2598 CCACCAGCTGAAGGGGGAGTACGAGGAGTGCACGCCCCACCAAGGAGCTGAACACCTC 2657
Qy      333  TCTGAACGACTC 344
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Db 2658 ACTGAACACACGC 2669

Search completed: December 13, 2005, 07:35:14
Job time : 153.309 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:13:57 ; Search time 739.984 Seconds
(without alignments)
7241.448 Million cell updates/sec

Title: US-09-977-579A-4_COPY_376_1023

Perfect score: 648

Sequence: 1 atcgctgccttcaatagatt.....cgggtaccagtgaggagaatag 648

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	648	100.0	1261	3	US-09-977-579-4
2	646.4	99.8	1261	9	US-10-482-834A-22
3	536.6	82.8	2220	3	US-08-977-579-3
4	536.6	82.8	2632	5	US-10-029-191-22
5	536.6	82.8	3195	9	US-10-029-191-1
6	534.8	82.5	1195	5	US-10-450-763-22568
7	534.6	82.5	645	5	US-10-029-191-21
8	392.6	60.6	3531	9	US-10-450-763-22567
9	362	55.9	600	10	US-11-060-756-2816
10	362	55.9	600	10	US-11-060-756-2817
11	362	55.9	600	10	US-11-060-756-7088
12	362	55.9	600	10	US-11-060-756-7089
13	229.2	35.4	545	4	US-09-925-065A-774904
14	224.4	34.6	621	9	US-10-450-763-22566
15	148.2	22.9	657	5	US-10-029-191-23
16	143.8	22.2	1275	10	US-11-060-756-3901
17	143.8	22.2	1275	8	US-11-060-756-8173
18	143.8	22.2	1335	8	US-10-723-860-2247
19	142.2	21.9	1414	8	US-10-477-272-1
20	142.2	21.9	1414	9	US-10-482-834A-11
21	142.2	21.9	1414	9	US-10-482-834A-12
22	141	21.8	407	7	US-10-276-774-718
23	138.6	21.4	1490	3	US-09-917-800A-1654

24	81.4	12.6	807	6	US-10-401-916-12	Sequence 12, Appl	
25	81.4	12.6	974	6	US-10-401-916-13	Sequence 13, Appl	
26	55	8.5	651	4	US-09-925-065A-513767	Sequence 513767, A	
27	55	8.5	651	4	US-09-925-065A-513768	Sequence 513768, A	
28	55	8.5	651	4	US-09-925-065A-513769	Sequence 513769, A	
29	51	7.9	502	4	US-09-925-065A-807996	Sequence 807996, A	
C	29	49	7.6	243	6	US-10-029-386-16214	Sequence 16214, A
30	49	7.6	569	6	US-10-029-386-2514	Sequence 2514, A	
31	49	7.6	3583	8	US-10-723-860-6471	Sequence 6471, Ap	
32	48.6	7.5	876	7	US-10-767-701-10747	Sequence 10747, A	
33	45.4	7.0	1645	9	US-10-647-517-29	Sequence 29, Appl	
34	45.4	7.0	954	8	US-10-425-115-100998	Sequence 100998, A	
C	35	45.2	7.0	495	4	US-09-925-065A-778585	Sequence 778585, A
36	45	6.9	496	4	US-09-925-065A-807954	Sequence 807954, A	
C	37	45	6.9	921	6	US-10-369-493-43050	Sequence 43050, A
38	44.8	6.8	53	9	US-10-491-192-5	Sequence 5, Appli	
C	39	44	6.8	60	9	US-10-491-192-6	Sequence 6, Appli
40	44	6.8	1434	6	US-10-259-194A-622	Sequence 622, App	
41	43.8	6.8	1720	7	US-10-425-114-19213	Sequence 19213, A	
42	43.8	6.8	1764	7	US-10-425-114-15538	Sequence 15538, A	
43	43.8	6.8	1794	7	US-10-425-114-25057	Sequence 25057, A	
44	43.8	6.8	2029	8	US-10-425-115-15884	Sequence 15884, A	
C	45	43.8	6.8			Sequence 15884, A	

ALIGNMENTS

RESULT 1
US-09-977-579-4

; Sequence 4, Application US/09977579

; Publication No. US20040248240A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod

; TITLE OF INVENTION: channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/977,579

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60,129,473

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-977-579-4

Query Match 100.0%; Score 648; DB 3; Length 1261;
Best Local Similarity 100.0%; Pred. No. 1.4e-200; Indels 0; Gaps 0;
Matches 648; Conservative 0; Mismatches 0;

Qy	1	ATGCCTCCCTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGGTCACT	60
Db	376	ATGCCTCCCTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTGGGTCACT	435
Qy	61	GTCTGTTCCCTGTGTGTGGAAAGTCCTCGGAGACGGAGCCGTGACGGGCAACCCC	120
Db	436	GTCTGTTCCCTGTGTGTGGAAAGTCCTCGGAGACGGAGCCGTGACGGGCAACCCC	495
Qy	121	ATGAGCTGCGTGCATCTCTGCATCAAGAGAGAGAGTGGAGCCACACCGTGGTG	180
Db	496	ATGAGCTGCGTGCATCTCTGCATCAAGAGAGAGAGTGGAGCCACACCGTGGTG	555
Qy	181	GAATGGTTCTACAGCCCGGAGGGCGGTAAAGATTTCCTTATTACAGATTCGGAATGGC	240
Db	556	GAATGGTTCTACAGCCCGGAGGGCGGTAAAGATTTCCTTATTACAGATTCGGAATGGC	615
Qy	241	CACGAGAGGTGGAGAGCCCTTTACGGGCGCTTCAGTGGAAATGGCAGCAAGACTG	300

Db 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTTCAGTGGAAATGGCAGCAAGGACCTG 675
Qy |||||
Db 301 CAGGACGTGTCATCAGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 360
Qy |||||
Db 676 CAGGACGTGTCATCAGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy |||||
Db 361 AATGTGTCCCGGAGTTTGTAGTTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
Qy |||||
Db 736 AATGTGTCCCGGAGTTTGTAGTTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795
Qy |||||
Db 421 ATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 480
Qy |||||
Db 796 ATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 855
Qy |||||
Db 481 ATGATGTACATCTCTCTGTCTTCTCCTCACCTGTGGCTGCTCATCGAGATATATATTC 540
Qy |||||
Db 856 ATGATGTACATCTCTCTGTCTTCTCCTCACCTGTGGCTGCTCATCGAGATATATATTC 915
Qy |||||
Db 541 TACGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTTGCC 600
Qy |||||
Db 916 TACGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTTGCC 975
Qy |||||
Db 601 ATCCCATCTGAGAACCAAGGAGACTCTCGGTACCAAGTGGAGGAATAG 648
Qy |||||
Db 976 ATCCCATCTGAGAACCAAGGAGACTCTCGGTACCAAGTGGAGGAATAG 1023

RESULT 2

US-10-482-834A-22

; Sequence 22, Application US/10482834A

; Publication No. US20050074764A1

; GENERAL INFORMATION:

; APPLICANT: Mulley, John Charles

; APPLICANT: Harbin, Louise Anne

; APPLICANT: Dibbens, Michelle

; APPLICANT: Wallace, Robyn

; APPLICANT: Phillips, Hillary Ann

; APPLICANT: Heron, Sara Elizabeth

; APPLICANT: Berkovic, Samuel Frank

; APPLICANT: Scheffer, Ingrid Eileen

; APPLICANT: Biomedics Limited

; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS

; FILE REFERENCE: 1386/17

; CURRENT APPLICATION NUMBER: US/10/482,834A

; CURRENT FILING DATE: 2004-01-02

; NUMBER OF SEQ ID NOS: 173

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 22

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-482-834A-22

Query Match 99.8%; Score 646.4; DB 9; Length 1261;
Best Local Similarity 99.8%; Pred. No. 4.7e-200;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTACTGGGTCAGT 60
Db 376 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTACTGGGTCAGT 435
Qy 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGCCGCTGAGGGCAACCCC 120
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGCCGCTGAGGGCAACCCC 495
Qy 121 ATGAAGCTGCGTGCATCTCTCGCATGAAGAGAGGAGGTGGAGGCCCAACACGTTG 180
Db 496 ATGAAGCTGCGTGCATCTCTCGCATGAAGAGAGGAGGTGGAGGCCCAACACGTTG 555
Qy 181 GAATGGTTCTACAGGCCCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGCG 240
Db 556 GAATGGTTCTACAGGCCCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGCG 615

Qy 241 CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTTCAGTGGAAATGGCAGCAAGGACCTG 300
Db 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTTCAGTGGAAATGGCAGCAAGGACCTG 675
Qy 301 CAGGACGTGTCATCAGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 360
Db 676 CAGGACGTGTCATCAGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 735
Qy 361 AATGTGTCCCGGAGTTTGTAGTTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
Db 736 AATGTGTCCCGGAGTTTGTAGTTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 795
Qy 421 ATCCCCCTAAGAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 480
Db 796 ATCCCCCTAAGAGTCACTGAGGAGGCTGGAGAGACTTCACTCTGTGGTCTCAGAAATC 855
Qy 481 ATGATGTACATCTCTCTGTCTTCTCCTCACCTGTGGCTGCTCATCGAGATATATATTC 540
Db 856 ATGATGTACATCTCTCTGTCTTCTCCTCACCTGTGGCTGCTCATCGAGATATATATTC 915
Qy 541 TACGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTTGCC 600
Db 916 TACGAAAGGTCTCAAAAGCCGAGAGGAGCCCAAGAAACGGGTCTGACTACCTTTGCC 975
Qy 601 ATCCCATCTGAGAACCAAGGAGACTCTCGGTACCAAGTGGAGGAATAG 648
Db 976 ATCCCATCTGAGAACCAAGGAGACTCTCGGTACCAAGTGGAGGAATAG 1023

RESULT 3

US-09-977-579-3

; Sequence 3, Application US/09977579

; Publication No. US20040248240A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod

; TITLE OF INVENTION: channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/977,579

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60,129,473

; PRIOR FILING DATE: 2000-02-24

; NUMBER OF SEQ ID NOS: 47

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 2220

; TYPE: DNA

; ORGANISM: rat

US-09-977-579-3

Query Match 82.8%; Score 536.6; DB 3; Length 2220;
Best Local Similarity 89.3%; Pred. No. 4.2e-164;
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 1 ATGCTGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTCTTATCTACTGGGTCAGT 60
Db 363 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTACTGGGTCAGA 422
Qy 61 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGCCGCTGAGGGCAACCCC 120
Db 423 GTCTGCTTCCCTGTGTGTGAAGTGCCTCGGAGAGGAGGTGGAGGCCCAACCTGTGGTG 482
Qy 121 ATGAAGCTGCGCTGCATCTCTCGCATGAAGAGAGGAGGTGGAGGCCCAACCGTGGTG 180
Db 483 ATGAAGCTGAGTGCATCTCTCGCATGAAGAGGAGGAGGTGGAGGCCCAACCTGTGGTG 542
Qy 181 GAATGGTTCTACAGGCCCGGCGGTAAAGATTTCTTATTTACGAGTATCGGAATGCG 240
Db 543 GAGTGGTTCTACAGGCCCTGAGGGCGGTAAAGATTTCTTATATATGAGTATCGGAATGCG 602

Qy 241 CACCAGAGGTGGAGAGCCCTTTCCAGGGCGCTGCAGTGGATGSCAGCAGGACCTG 300
Db |||||
Qy 603 CACCAGGAAGTGGAGAGCCCTTTCCAGGGCGCTGCAGTGGATGSGAGCAAGACCTG 662
Db |||||
Qy 301 CAGGACGTGTCCATCACTGTGCTCAAGGTCACTCTGAACGACTCTGGCCCTTACACCTGC 360
Db |||||
Qy 663 CAGGACGTATCCATCACTGTACTCAATGTCACTTTGAATGACTCTGGCCCTTACACATGC 722
Db |||||
Qy 361 AATGTGTCGGGAGTTTGAAGTGGAGCGCATCGGCCCTTTTGAAGAGACGCGGCTG 420
Db |||||
Qy 723 AATGTGTCAGGGAGTTTGAATTCAGGCAACACAGGCGCTTTTGTGAAGACACACGACTG 782
Db |||||
Qy 421 ATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGACTTCACCTCTGTGGTCTCAGAATC 480
Db |||||
Qy 783 ATACCTTTGGAGTCACTGAAGAGCGGGAAGACTTCACCTCCGGTGGTCTCGAAATC 842
Db |||||
Qy 481 ATGATGTACATCTCTGGTCTTCTCAACCTGTGGCTGCTCATCGAGATGATATATGC 540
Db |||||
Qy 843 ATGATGTACATCTCTGGTCTTCTCACTGTGGCTGTTTATGAGATGATATATGC 902
Db |||||
Qy 541 TACAGAAAGGTCTCAAAAGCCGAAGAGCGAGCCCAAGAAACCGCTCTGACTACCTTGGC 600
Db |||||
Qy 903 TACAGAAAGGTCTCTAAGGCCGAAGAGCGAGCACAGGAAATGCTCTGACTACCTTGGT 962
Db |||||
Qy 601 ATCCCATCTGAGAACACAGGAGAACTCTGCGTACCACTGAGGGAATA 647
Db |||||
Qy 963 ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTCTGGAGGAATA 1009
Db |||||

RESULT 4

US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Query Match 82.8%; Score 536.6; DB 5; Length 2632;
Best Local Similarity 89.3%; Pred. No. 4.5e-164;
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 1 ATGCTGCTTCAATAGATTCTTCCCTGGCTTCTCTCGTGTATCTACTGGTTCAGT 60
Db |||||
Qy 78 ATGCTGCTTCAACAGATTCTTCCCTAGCTTCTCTAGTGTCTATCTACTGGTTCAGA 137
Db |||||
Qy 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACGGAGCGCTGCAGGGCAACCCC 120
Db |||||
Qy 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACAGAAGCGGTGCAGGGCAATCCC 197
Db |||||
Qy 121 ATGAAGTGCCTGCATCTCTGATGAAGAGAGAGGTGGAGGCCACACCGTGGTG 180
Db |||||
Qy 198 ATGAAGTGCAGTGCATCTCTGATGAAGAGAGAGGTGGAGGCCACACCTGTGGTG 257
Db |||||
Qy 181 GAATGGTTCTACAGCCCGGCGGTAAAGATTCTTATTTACGAGTATCGGAATGGC 240
Db |||||
Qy 258 GAGTGGTTCTACAGCCCTGAGGGCGGTAAAGATTCTTATATATGATATCGGAATGGC 317
Db |||||
Qy 241 CACCAGGAGTGGAGAGCCCTTTTCAGGGCGCTGTCAGTGGATGGCAGGACCTG 300
Db |||||

Db 318 CACCAGGAAGTGGAGAGCCCTTTCCAGGGCGCTTCAGTGGATGGAGCAAGACCTG 377
Qy |||||
Qy 301 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCCTTACACCTGC 360
Db |||||
Qy 378 CAGGACGTATCCATCACTGTACTCAATGTCACTTTGAATGACTCTGGCCCTTACACATGC 437
Db |||||
Qy 361 AATGTGTCGGGAGTTTGAAGTGGAGCGCATCGGCCCTTTTGAAGAGACGCGGCTG 420
Db |||||
Qy 438 AATGTGTCAGGGAGTTTGAATTCAGGCAACACAGGCGCTTTTGTGAAGACACACGACTG 497
Db |||||
Qy 421 ATCCCCCTAAGAGTCACCGAGGAGCTGGAGAGACTTCACCTCTGTGGTCTCAGAATC 480
Db |||||
Qy 498 ATACCTTTGGAGTCACTGAAGAGCGGGAAGACTTCACCTCCGGTGGTCTCGAATC 557
Db |||||
Qy 481 ATGATGTACATCTCTGGTCTTCTCAACCTGTGGCTGCTCATCGAGATGATATATGC 540
Db |||||
Qy 558 ATGATGTACATCTCTGGTCTTCTCACTGTGGCTGTTTATGAGATGATATATGC 617
Db |||||
Qy 541 TACAGAAAGGTCTCAAAAGCCGAAGAGCGAGCCCAAGAAACCGCTCTGACTACCTTGGC 600
Db |||||
Qy 618 TACAGAAAGGTCTCTAAGGCCGAAGAGCGAGCACAGGAAATGCTCTGACTACCTTGGT 677
Db |||||
Qy 601 ATCCCATCTGAGAACACAGGAGAACTCTGCGGTACCACTGAGGGAATA 647
Db |||||
Qy 678 ATCCCTTCAGAGAACAGGAGAACTCTGTGGTACCTCTGGAGGAATA 724
Db |||||

RESULT 5

US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A. J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Query Match 82.8%; Score 536.6; DB 5; Length 3108;
Best Local Similarity 89.3%; Pred. No. 4.8e-164;
Matches 578; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 1 ATGCTGCTTCAATAGATTCTTCCCTGGCTTCTCTCGTGTATCTACTGGTTCAGT 60
Db |||||
Qy 78 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTATCTACTGGTTCAGA 137
Db |||||
Qy 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACGGAGCGCTGCAGGGCAACCCC 120
Db |||||
Qy 138 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACAGAAGCGGTGCAGGGCAATCCC 197
Db |||||
Qy 121 ATGAAGTGCCTGCATCTCTGATGAAGAGAGAGGTGGAGGCCACACCGTGGTG 180
Db |||||
Qy 198 ATGAAGTGCAGTGCATCTCTGATGAAGAGAGAGGTGGAGGCCACACCTGTGGTG 257
Db |||||
Qy 181 GAATGGTTCTACAGCCCGGCGGTAAAGATTCTTATTTACGAGTATCGGAATGGC 240
Db |||||
Qy 258 GAGTGGTTCTACAGCCCTGAGGGCGGTAAAGATTCTTATATATGATATCGGAATGGC 317
Db |||||
Qy 241 CACCAGGAGTGGAGAGCCCTTTTCAGGGCGCTGTCAGTGGATGGCAGGACCTG 300
Db |||||

Db 318 CACCAGGAAGTGGAGAGCCCTTCAAGGCCGTCTGCAGTGAATGGAGCAAGACCTG 377
Qy 301 CAGACGTGTCCATCAGTGTCTCAACGTCTACTCTGAACGACTCTGGCCCTCTACACCTGC 360
Db 378 CAGGACGTATCCATCACTGTACTCAATGTCTACTTTGAATGACTCTGGCCCTCTACACATGC 437
Qy 361 AATGTGTCCTCCGGAGTTTGTAGTTTGTAGCGCATCGGCCCTTTGTGAAGACGACCGGCTG 420
Db 438 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCTTTTGTGAAGACACAGACTG 497
Qy 421 ATCCCCCTTAAGACTCACCGAGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 480
Db 498 ATACCTTTGCGAGTCACTGAAGAGGCGGAGAACTTCACCTCCGTGGTCTCGGAAATC 557
Qy 481 ATGATGTACATCTCTGTGCTTCTTCTCACCCTGTGGCTGCTCATCGAGATGATATATGC 540
Db 558 ATGATGTACATCTCTGTGCTTCTTCTCACCCTGTGGCTGTTTATTTGAGATGATCTATTGC 617
Qy 541 TACAGAAAGGTCTCAAAAGCCGAAGAGCGACGCCCAAGAAACGCGTCTGACTACTTTGCC 600
Db 618 TACAGAAAGGTCTCTAAGCCCGAAGAGCAGCAGAGAAATGCGTCTGACTACTTTGCT 677
Qy 601 ATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACCGTACCGTGGAGGAATA 647
Db 678 ATCCCTTCAGAGAACAAAGGAGAACTCTGTGTACTCTGTGGAGGAATA 724

RESULT 6

US-10-450-763-22568
; Sequence 22568, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22568
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (518)..(1051)
; OTHER INFORMATION: 91% homologous to Homo sapiens voltage-gated sodium channel
; OTHER INFORMATION: beta-3 subunit, accession number AJ243396, Smith-Waterman Score=826
US-10-450-763-22568

Query Match 82.5%; Score 534.8; DB 9; Length 1195;
Best Local Similarity 95.7%; Pred. No. 1.3e-163;
Matches 572; Conservative 0; Mismatches 22; Indels 4; Gaps 2;
Qy 1 ATGCTGCTCCCTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTTATCTACTGGGTCACT 60
Db 463 ATGCTGCTCCCTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTTATCTACTGAGTCACT 522
Qy 61 GTCTGCTTCCCTGTGTGTGTGAA--GTGCGCTCGGACGAGAGCCGTGCA--GGGCAA 116
Db 523 GTCTGCTTCCCTGTGTGTGGGGAAGTGCCTTTAGAAAACGGGGCGGCGACGGCTAA 582
Qy 117 CCCCATGAAGCTGCCCTGATCTCTGATGAAGAGAGAGGAGGTGGAGGCCACACCGGT 176
Db 583 CCCCATGAAGCTGCCCTGATCTCTGATGAAGAGAGAGGAGGTGGAGGCCACACCGGT 642
Qy 177 GGTGGAATGGTTCTACAGCCCGGCGGTAAAGATTTCCTTATTACGAGTATCGGAA 236

Db 643 GGTGGAATGGTTCTACAGGCCCGGCGGTAAAGATTTCCTTATTACGAGTATCGAA 702
Qy 237 TGGCCACCAGAGGTGGAGAGCCCTTTTCAAGGGCGCTCGAGTGAATGGCAGCAAGGA 296
Db 703 TGGCCACCAGAGGTGGAGAGCCCTTTTCAAGGGCGCTCGAGTGAATGGCAGCAAGGA 762
Qy 297 CTGTCAGAGGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTGGCCCTCTACAC 356
Db 763 CTGTCAGAGGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTGGCCCTCTACAC 822
Qy 357 CTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGGCGCATCGGCCCTTTGTGAAGACGACGCG 416
Db 823 CTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGGCGCATCGGCCCTTTGTGAAGACGACGCG 882
Qy 417 GCTGATCCCCCTTAAGAGTCAACGAGAGGCTGGAGAGGACTTCACCTCTGTGTCTCAGA 476
Db 883 GCTGATCCCCCTTAAGAGTCAACGAGAGGCTGGAGAGGACTTCACCTCTGTGTCTCAGA 942
Qy 477 AATCATGATGTACATCTCTGTGTCTTCTCACCCTGTGGCTGCTCATCGAGATGATATA 536
Db 943 AATCATGATGTACATCTCTGTGTCTTCTCACCCTGTGGCTGCTCATCGAGATGATATA 1002
Qy 537 TTGCTACAGAAAGGTCTCAAAAGCCGAAGAGCGAGCCCAAGAAAACCGCTCTGACTAC 594
Db 1003 TTGCTACAGACAGGTCTCAAAAGCCGAAGAGCGAGCCCAAGAAAACCGCGCAGGAAAC 1060

RESULT 7

US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-21

Query Match 82.5%; Score 534.6; DB 5; Length 645;
Best Local Similarity 89.3%; Pred. No. 1.2e-163;
Matches 576; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
Qy 1 ATGCTGCTCCCTCAATAGATTGTTTCCCTCGCTTCTCTCGTCTTATCTACTGGGTCACT 60
Db 1 ATGCTGCTCCCTCAACAGATTGCTTCCCTAGCTTCTCTAGTGCTCATCTACTGGTTCAGA 60
Qy 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGGAGCGCGTGCAGGGCAACCCC 120
Db 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGGAGACAGAGCGGTGCAGGGCAATCCC 120
Qy 121 ATGAAGTGGCTGCATCTCTGCAATGAAGAGAGAGAGGTGGAGGCCACACCGTGGTG 180
Db 121 ATGAAGTGGAGTGCATCTCTGCAATGAAGAGGAGAGGTGGAGGCCACACCTGTGGTG 180
Qy 181 GAATGGTCTACAGCCCGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGCG 240
Db 181 GAGTGGTCTACAGCCCTGAGGGCGGTAAAGATTTCCTTATATGATATCGGAATGCG 240
Qy 241 CACCAGGAGGTGGAGAGCCCTTTTCAGGGCGCTCGAGTGGAAATGGCAGCAAGACCTG 300

Db 241 CACAGGAAGTGGAGAGCCCTTCCAAAGCCGCTCTGCAGTGGAAATGGAGCAAGACCTG 300
Qy 301 CAGGACGTGTCCATCACTGTGCTCAAGCTCACTCTGAACGACTCTGGCCCTCTACACCTGC 360
Db 301 CAGGACGTATCCATCACTGTACTCAATGTCACTTTGAATGACTCTGGCCCTACACATGC 360
Qy 361 AATGTGTCCGGAGTTTGTAGTTGAGCGCATCGGCCCTTTGTGAAGACGACGCGCTG 420
Db 361 AATGTGTCCAGGGAGTTTGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCCAGAGACTG 420
Qy 421 ATCCCCCTTAAGAGTCAACGAGAGGCTGGAGAGACTTCACTCTGTGTCTCAGAAATC 480
Db 421 ATACCTTTGGAGTCACTGAAGAGCGGAGAGACTTCACTCTCGTGGTCTCGAAATC 480
Qy 481 ATGATGTACATCTCTTGTGCTTCTCCTCACCCCTGTGGCTGTCTCATCGAGATGATATTCG 540
Db 481 ATGATGTACATCTCTCTGCTTCTCCTCACCTTGTGGCTGTTTATTGAGATGATCTATTGC 540
Qy 541 TACAGAAAGTCTCAAAAGCCGAAGAGCGACGCCCAAGAAAGCGTCTGACTACCTTGGC 600
Db 541 TACAGAAAGTCTCTAAAGCCGAAGAGCGACGACAGGAAATGCGTCTGACTACCTTGTCT 600
Qy 601 ATCCCATCTGAGAACAAAGGAGAACTCTGCGGTACACAGTGGAGGAA 645
Db 601 ATCCCTTCAGAGAACAAAGGAGAACTCTGTGTACCTGTGTGGAGGAA 645

RESULT 8
US-10-450-763-22567
; Sequence 22567, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22567
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (300)..(407)
; OTHER INFORMATION: 94% homologous to Homo sapiens putative kruppel-related zinc
; OTHER INFORMATION: finger protein NY-REN-23 antigen, accession number AF155101, Smith-
US-10-450-763-22567

Query Match 60.6%; Score 392.6; DB 9; Length 3531;
Best Local Similarity 99.0%; Pred. No. 5.4e-117;
Matches 395; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 47 TCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCCG 106
Db 2951 TCAGGTGTGTGAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGACGAGGCCG 3010
Qy 107 TGCAGGCAACCCCATGAAGTGGCTGCAATCTCTCATGAAGAGAGAGGTGGAG 166
Db 3011 TGCAGGCAACCCCATGAAGTGGCTGCAATCTCTCATGAAGAGAGAGGTGGAG 3070
Qy 167 CCACACGGTGGTGGATGTTCTACAGGCCGAGGGCGGTAAAGATTCTTTATTACG 226
Db 3071 CCACACGGTGGTGGATGTTCTACAGGCCGAGGGCGGTAAAGATTCTTTATTACG 3130

Qy 227 AGTATCGGAATGGCCACCAGGAGGTGGAGAGCCCTTTTCAGGGCGGCTGCAGTGGGAATG 286
Db 3131 AGTATCGGAATGGCCACCAGGAGGTGGAGAGCCCTTTTCAGGGCGGCTGCAGTGGGAATG 3190
Qy 287 GCAGCAGGACCTGCAGGAGCTGTCCATCACTGTGTCTCAACGTCACCTCTGAACGACTCTG 346
Db 3191 GCAGCAGGACCTGCAGGAGCTGTCCATCACTGTGTCTCAACGTCACCTCTGAACGACTCTG 3250
Qy 347 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGGCGCATCGGCCCTTTGTGA 406
Db 3251 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGGCGCATCGGCCCTTTGTGA 3310
Qy 407 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGG 445
Db 3311 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGG 3349

RESULT 9
US-11-060-756-2816
; Sequence 2816, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2816
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2816

Query Match 55.9%; Score 362; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 287 GCAGCAGGACCTGCAGGAGCTGTCCATCACTGTGTCTCAACGTCACCTCTGAACGACTCTG 346
Db 1 GCAGCAGGACCTGCAGGAGCTGTCCATCACTGTGTCTCAACGTCACCTCTGAACGACTCTG 60
Qy 347 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGGCGCATCGGCCCTTTGTGA 406
Db 61 GCCTCTACACCTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGGCGCATCGGCCCTTTGTGA 120
Qy 407 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTTCACCTCTG 466
Db 121 AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTTCACCTCTG 180
Qy 467 TGTCTCAGAAATCATGATGATCATCTTCTGTGTCTTCTCACCCTGTGGCTGTCTATCG 526
Db 181 TGTCTCAGAAATCATGATGATCATCTTCTGTGTCTTCTCACCCTGTGGCTGTCTATCG 240
Qy 527 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAACCGT 586
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAACCGT 300
Qy 587 CTGACTACCTTGGCATCCCATCTGAGAAACAGGAGAACTCTGGGGTACCAAGTGGAGGAAT 646
Db 301 CTGACTACCTTGGCATCCCATCTGAGAAACAGGAGAACTCTGGGGTACCAAGTGGAGGAAT 360
Qy 647 AG 648
Db 361 AG 362

RESULT 10
US-11-060-756-2817
; Sequence 2817, Application US/11060756

Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817

Query Match 55.9%; Score 362; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	287	GCAGCAAGGACCTGCAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	346
Db	1	GCAGCAAGGACCTGCAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	60
Qy	347	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	406
Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	120
Qy	407	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	466
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	180
Qy	467	TGGTCTCAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	526
Db	181	TGGTCTCAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	240
Qy	527	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCCCAAGAAACGGT	586
Db	241	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCCCAAGAAACGGT	300
Qy	587	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	646
Db	301	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	360
Qy	647	AG 648	
Db	361	AG 362	

RESULT 11
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088

Query Match 55.9%; Score 362; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	287	GCAGCAAGGACCTGCAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	346
Db	1	GCAGCAAGGACCTGCAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	60
Qy	347	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	406
Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	120
Qy	407	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	466
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	180
Qy	467	TGGTCTCAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	526
Db	181	TGGTCTCAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	240
Qy	527	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCCCAAGAAACGGT	586
Db	241	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCCCAAGAAACGGT	300
Qy	587	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	646
Db	301	CTGACTACCTTGCATCCCATCTGAGAAACAGGAGAACTCTGCGGTACCACTGGAGGAAT	360
Qy	647	AG 648	
Db	361	AG 362	

RESULT 12
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Query Match 55.9%; Score 362; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.8e-107;
Matches 362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	287	GCAGCAAGGACCTGCAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	346
Db	1	GCAGCAAGGACCTGCAGGACGTGTCATCACTGTGCTCAACGTCACCTCTGAACGACTCTG	60
Qy	347	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	406
Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGA	120
Qy	407	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	466
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACTCTG	180
Qy	467	TGGTCTCAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	526
Db	181	TGGTCTCAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	240
Qy	527	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCCCAAGAAACGGT	586
Db	241	AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGCGCAGCCCAAGAAACGGT	300

Qy 587 CTGACTACCTTGCATCCCATCTGAGAACAGGAGAACTCTGCGGTACCAAGTGAGGAAT 646
Db 301 CTGACTACCTTGCATCCCATCTGAGAACAGGAGAACTCTGCGGTACCAAGTGAGGAAT 360
Qy 647 AG 648
Db 361 AG 362

RESULT 13

US-09-925-065A-774904
; Sequence 774904, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774904
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-774904

Query Match 35.4%; Score 229.2; DB 4; Length 545;
Best Local Similarity 95.9%; Pred. No. 6.4e-64;
Matches 234; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 212 ATTTCTCTATTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGC 271
Db 136 ATCTGCAGATTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGC 195
Qy 272 GCCTGCAGTGAATGGCAGCAAGGACCTGCGAGGACGTGTCCATCACTGTGCTCAACGTCA 331
Db 196 GCCTGCAGTGAATGGCAGCAAGGACCTGCGAGGACGTGTCCATCACTGTGCTCAACGTCA 255
Qy 332 CTCTGAACGACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGGTTGAGGGGC 391
Db 256 CTCTGAACGACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGGTTGAGGGGC 315
Qy 392 ATCGGCTCTTTGAAGACGACGCGGTGTATCCCTTAAGAGTCAACGAGGAGCTGGAG 451
Db 316 ATCGGCTCTTTGAAGACGACGCGGTGTATCCCTTAAGAGTCAACGAGGAGGTGAGG 375
Qy 452 AGGA 455
Db 376 CTGA 379

RESULT 14

US-10-450-763-22566
; Sequence 22566, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763

; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22566
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (40)..(282)
; OTHER INFORMATION: 95% homologous to Rattus norvegicus voltage-gated sodium
; OTHER INFORMATION: channel beta-3 subunit, accession number AJ243395, Smith-Waterman
; OTHER INFORMATION: Score=397.
US-10-450-763-22566

Query Match 34.6%; Score 224.4; DB 9; Length 621;
Best Local Similarity 99.6%; Pred. No. 2.5e-62;
Matches 225; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 220 ATTTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAG 279
Db 58 ATTTACGAGTATCGGAATGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTGCAG 117
Qy 280 TGGATGGCAGCAAGGACCTGCGAGGAGTGTCCATCACTGTGCTCAACGTCTCAAC 339
Db 118 TGGATGGCAGCAAGGACCTGCGAGGAGTGTCCATCACTGTGCTCAACGTCTCAAC 177
Qy 340 GACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGAGTTGAGGGCGCATCGGCC 399
Db 178 GACTCTGGCTCTACACCTGCAATGTCTCCGGAGTTTGAGTTGAGGGCGCATCGGCC 237
Qy 400 TTTGTGAAGACGACGCGGCTGTATCCCTTAAGAGTCAACGAGGAGG 445
Db 238 TTTGTGAAGACGACGCGGCTGTATCCCTTAAGAGTCAACGAGGAGG 283

RESULT 15

US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/SUI
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Lepus Sp.
US-10-029-191-23

Query Match 22.9%; Score 148.2; DB 5; Length 657;
Best Local Similarity 57.7%; Pred. No. 2e-37;
Matches 333; Conservative 0; Mismatches 223; Indels 21; Gaps 3;

Qy 76 TGTGTGAAGTCCCTCGGAGACGAGGCGGTGGAGGACCCCATCAACCTGCGCTGC 135
Db 61 TGCCTGGAGGTGGACTCGGAGACCGGCGGTGACCGGATGACCTTCAAAATTTGTGC 120

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:25:32 ; Search time 174.718 Seconds
(without alignments)
1386.561 Million cell updates/sec

Title: US-09-977-579A-4_COPY_376_1023

Perfect score: 648

Sequence: 1 atgcctgcctcaatagatt.....cggataccagtgagggaatag 648

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.*

- 1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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- 5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	648	100.0	1261	6	US-10-374-954-8
2	143.8	22.2	1335	6	US-10-374-954-4
3	130.4	20.1	880	6	US-10-750-185-44336
4	57.8	8.9	1497	6	US-10-750-185-44339
5	51	7.9	150468	7	US-11-112-908-56
6	51	7.9	193789	7	US-11-112-908-55
7	38	5.9	1689	6	US-10-507-928-9
8	38	5.9	1689	6	US-10-507-928-11
9	38	5.9	1689	7	US-11-029-465-9
10	38	5.9	1689	7	US-11-029-465-11
11	36.2	5.6	673	7	US-11-080-991-111
12	36.2	5.6	1371	6	US-10-131-826A-487
13	35.4	5.5	2849	6	US-10-131-826A-371
14	34	5.2	175100	7	US-11-121-086-21
15	33.8	5.2	1485	6	US-10-750-185-61749
c 16	32.8	5.1	1506	6	US-10-750-185-30397
c 17	32.8	5.1	2236	6	US-10-131-826A-381
18	32.4	5.0	33737	6	US-10-276-233A-7
c 19	32.4	5.0	162085	7	US-11-121-086-7
20	32.2	5.0	4104	6	US-10-131-826A-449
21	32	4.9	762	6	US-10-821-234-586
c 22	32	4.9	2257	6	US-10-750-185-46007
23	31.8	4.9	2454	6	US-10-750-185-30593

ALIGNMENTS

RESULT 1

US-10-374-954-8

; Sequence 8, Application US/10374954

; Publication No. US20050260576A1

; GENERAL INFORMATION:

; APPLICANT: Vanderbilt University

; APPLICANT: George, Alfred L.

; APPLICANT: Lossin, Christoph

; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN

; FILE REFERENCE: 1242/41/2

; CURRENT APPLICATION NUMBER: US/10/374,954

; PRIOR FILING DATE: 2003-02-25

; PRIOR FILING DATE: 2002-02-25

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 8

; LENGTH: 1261

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (376)..(1023)

US-10-374-954-8

Query Match 100.0%; Score 648; DB 6; Length 1261;

Best Local Similarity 100.0%; Pred. No. 9.5e-181;

Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCCTTCAATAGATTGTTTCCCTGCGTCTCTCGTCTTCTACTGCGTCACT 60

Db 376 ATGCTGCCTTCAATAGATTGTTTCCCTGCGTCTCTCGTCTTCTACTGCGTCACT 435

Qy 61 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACGGAGCGCGTGCAGGGCAACCCC 120

Db 436 GTCTGCTTCCCTGTGTGTGGAAGTGCCTTCGAGACGGAGCGCGTGCAGGGCAACCCC 495

Qy 121 ATGAAGTGGCGTGCATCTCTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180

Db 496 ATGAAGTGGCGTGCATCTCTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 555

Qy 181 GAATGGTTTACAGGGCGGCGGTAAGATTTCCTTATTTACGAGTATCGGAATGGC 240

Db 556 GAATGGTTTACAGGGCGGCGGTAAGATTTCCTTATTTACGAGTATCGGAATGGC 615

Qy 241 CACCAGAGGTGGAGAGCCCTTTTCAGGGGGCCCTGACAGTGAATGGCAGCAAGACCTG 300
Db |||||
616 CACCAGAGGTGGAGAGCCCTTTTCAGGGGGCCCTGACAGTGAATGGCAGCAAGACCTG 675
Qy 301 CAGGACGTGTCATCAGTGTGCTAACTCACTCTGAAACGACTCTGGGCTTCAACCTGC 360
Db |||||
676 CAGGACGTGTCATCAGTGTGCTAACTCACTCTGAAACGACTCTGGGCTTCAACCTGC 735
Qy 361 AATGTGTCCTGGGAGTTTGGTTTGGAGCGCATCGGCCCTTTTGGAGACGACCGGCTG 420
Db |||||
736 AATGTGTCCTGGGAGTTTGGTTTGGAGCGCATCGGCCCTTTTGGAGACGACCGGCTG 795
Qy 421 ATCCCCCTAAGAGTCACCCAGAGGCTCGAGAGGACTTCACTCTGTGGTCTCAGAAATC 480
Db |||||
796 ATCCCCCTAAGAGTCACCCAGAGGCTCGAGAGGACTTCACTCTGTGGTCTCAGAAATC 855
Qy 481 ATGATGATACCTTCTGCTTCTTCACTACCTGTGGCTGCTCATCGAGATGATATATGC 540
Db |||||
856 ATGATGATACCTTCTGCTTCTTCACTACCTGTGGCTGCTCATCGAGATGATATATGC 915
Qy 541 TACAGAAAGTCTCAAAAGCCGAGAGCGACGCCCAAGAAACGGCTCTGACTACCTTGGC 600
Db |||||
916 TACAGAAAGTCTCAAAAGCCGAGAGCGACGCCCAAGAAACGGCTCTGACTACCTTGGC 975
Qy 601 ATCCCATCTGAGAAACAGGAGAACTCTCGCGTACAGTGGAGGAATAG 648
Db |||||
976 ATCCCATCTGAGAAACAGGAGAACTCTCGCGTACAGTGGAGGAATAG 1023

RESULT 2
US-10-374-954-4
; Sequence 4, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(681)
US-10-374-954-4

Query Match 22.2%; Score 143.8; DB 6; Length 1335;
Best Local Similarity 56.9%; Pred. No. 1e-32; Indels 21; Gaps 3;
Matches 334; Conservative 0; Mismatches 232;
Qy 66 CTTCCCTGTGTGTGGAAGTGCCTTCGGAGACGAGGCGCGTGCAGGGGCAACCCCATGAA 125
Db |||||
75 CTGCGGGGCTGCGTGGAGGTGGACTCGGAGACCGAGCGCGTGTATGGATGACCTTCAA 134
Qy 136 GCTCGCTGCTATCTCTGATGATGAAGAGAGAGAGGTGGAGGCCACACGCGTGGTGAATG 185
Db |||||
135 AATCTTTGTCATCTCTGCAAGCGCGCAGCGAGCACCACGCTGAGACCTTCAACCGAGTG 194
Qy 186 GTTCTACAGGCCCGAGGGCGTAAAGATT-----TCTTATTTACGAGTATCGAA 236
Db |||||
195 GACCTTCGCCAGAGAGGGCACTGAGAGTTTGTCAAGATCTTCGCCCTATGAGAAATGAGGT 254
Qy 237 TGGCCACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTTCAGTGGAAATGGCAG----- 290
|||

Db 255 GTTGCAGCTGGAGAGGATGAGCGCTTCGAGGGCCGCTGTGTGGAATGGCAGCCGGGG 314
Qy 291 ---CAAGGACCTCGAGGACGTGTCCATCACTGTGTCTCAAGCTCACTCTGAACGACTCTGG 347
Db |||||
315 CACCAAGACCTCGAGGATCTGTCTTCTCATCACCATGTACCTTACCAACCACTCGGG 374
Qy 348 CCTCTACACCTGCAATGTGTCCCGGAGTTTGAAGTTTGAAGCGCATCGGCCCTTTTGTGAA 407
Db |||||
375 CGACTACGAGTGCACCGTCTACCGCTGCTCTTCTTCGAAAACTACGAGCACAACACGAG 434
Qy 408 GAGACCGCGGTATCCCTCAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGT 467
Db |||||
435 CGTCGTCAAGAAGATCCACATTTGAGGTAGTGGCAAAAGCCCAACAGAGACATGGCATCAT 494
Qy 468 GGTCTCAGAAATCATGATGTACATCCTCTGTGTTCTTCTCACCCTGTGGTGTCTATCGA 527
Db |||||
495 CGTCTGTGAGATCATGATGTATGTGCTCATTTGGTGTTCACCNATATGGTCTGGGAGA 554
Qy 528 GATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGAG---GCAGCCCAAGAAAAACGC 584
Db |||||
555 GATGATTTACTGTCTACAAGAAGATCGCTGCCGCCACGAGAGCTGCTGCACAGGAGATGC 614
Qy 585 GTCTGACTACTTGGCCATCCCATCTGAGAAACAAGGAGAACTCTGCGG 631
Db |||||
615 CTCGGAATAGCTGGCCATCACCTCTGAAAGCAAAAGAGAACTGCACGG 661

RESULT 3
US-10-750-185-44336
; Sequence 44336, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 44336
; LENGTH: 880
; TYPE: DNA
; ORGANISM: Bovine
; ORGANISM: Bovine 19866880898198
US-10-750-185-44336

Query Match 20.1%; Score 130.4; DB 6; Length 880;
Best Local Similarity 82.8%; Pred. No. 7.3e-29;
Matches 149; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 414 CGCGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGGACTTCACTCTGTGGTCTC 473
Db |||||
412 GCGCATTTCTGAGTCTCATTTCTCTCCCTTGCAGCTGGAGAGGACTTCACTCTGTGGTCTC 471
Qy 474 AGAATCATGATGTACATCTTCTGTGTTCTTCTCACCCTGTGGTGTCTCATCGAGATGAT 533
Db |||||
472 AGAATCATGATGTACATCTCTCTGTTCTTCTCTCTCTCTGTGGTGTCTCATTTGAGATGAT 531
Qy 534 ATATTGCTACAGAAAGGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAAAACGCGTCTGACTA 593
Db |||||
532 ATATTGCTACAGGAAGGTCTCGAAGGCTGAAGAGGCGGCCCAAGAAAAATGCTTAAGTCCA 591

RESULT 4
US-10-750-185-44339
; Sequence 44339, Application US/10750185

Db 52662 AATTCTTTGCACTCTCTCGAAGCGCGGACGAGGACCAACCGTGTAGACCTTCACCGAGTG 52721

Qy 186 GTTCTACAGGCCGAGGCGGTAAAGATTTTCCTTA 220

Db 52722 GACCTTCGCCAGAAGGCGCACTGAGGAGTTGTCA 52756

RESULT 6

US-11-112-908-55

; Sequence 55, Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Davis, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 55

; LENGTH: 193789

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-55

Query Match 7.9%; Score 51; DB 7; Length 193789;

Best Local Similarity 58.1%; Pred. No. 0.00012; Indels 0; Gaps 0;

Matches 90; Conservative 0; Mismatches 65;

Qy 66 CTTCCCTGTGTGTGGAAGTGCCTCGGAGACGGAGGCGCGTGCAAGGCGCAACCCCATGAA 125

Db 102787 CTGCGGGGCTGCGTGGAGTGGACTCGGAGACCGAGGCCGCTGTATGGATGACCTTCAA 102846

Qy 126 GCTCGGTGCACTCTCTGCATGAAGAGAGAGAGGTGGAGGCCACCGCGTGGTGAATG 185

Db 102847 AATTCTTTGCACTCTCTCGAAGCGCGGACGAGACCAACCGTGTAGACCTTCACCGAGTG 102906

Qy 186 GTTCTACAGGCCGAGGCGGTAAAGATTTTCCTTA 220

Db 102907 GACCTTCGCCAGAAGGCGCACTGAGGAGTTGTCA 102941

RESULT 7

US-10-507-928-9

; Sequence 9, Application US/10507928

; Publication No. US20050266024A1

; GENERAL INFORMATION:

; APPLICANT: POWDERMED LIMITED AND GLAXO GROUP LIMITED

; TITLE OF INVENTION: ADJUVANT

; FILE REFERENCE: N 88232B GCW

; CURRENT APPLICATION NUMBER: US/10/507,928

; CURRENT FILING DATE: 2004-09-17

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 1689

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: nucleotide sequence of RT insert of p7077-RT3

US-10-507-928-9

Query Match 5.9%; Score 38; DB 6; Length 1689;

Best Local Similarity 62.8%; Pred. No. 0.13;


```
; Best Local Similarity 47.9%; Pred. No. 0.89;
Matches 102; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 105 CGTCAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGCAATGAAGAGAGGAGGTGGA 164
Db 898 CGTCACACCTGGAAACCAAGAGGAGACCTACTCTGCATCATGAAGAACGAGGAGGT 957
Qy 165 GGCACACACGCTGGTGGAAATGGTCTACAGGCCCGAGGGCGTAAAGATTTCCTTATTTA 224
Db 958 GGTGATCTTGTTCGGCAGGTGGGGACCGCAGCATATGCAAAAGCCAGAGCCTGATGCT 1017
Qy 225 CGAGTATCGGAATGGCCACAGGAGGTGGAGAGCCCTTTTCAGGGGCGCCTGCGATGGAA 284
Db 1018 GGAGCTCGAGAGCAGGACCAAGGTGTGGTACGCTCTTACAAGGGCGCAACGTGAGAACGC 1077
Qy 285 TGGCAGCAAGACCTGCGAGGAGCTGTCCATCAC 317
Db 1078 CATCTTCAGCGAGGAGCTGGACACCTATCATAC 1110
```

```
RESULT 14
US-11-121-086-21
; Sequence 21, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138-6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 175100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-21
```

```
Query Match 5.2%; Score 34; DB 7; Length 175100;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 70; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 43 CTTATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGTGGAGTCCCTCGAGACGGAG 102
Db 81718 CTGGTGTGCTGATCAGTGACTTCTACCCGGGAGCTGTGAAAGTGGCCTGGAAGGCAGAT 81777
Qy 103 GCGGTGCGAGGGCAACCCCATGAAGCTGCGCTGCATCTCTGCATGAAGAGAGAGGAGTG 162
Db 81778 GGCAGCCCGTCAACGGGGAGTGGAGACCACACCTCTCAACACAGAGCAACACAG 81837
Qy 163 GAGGCCACCA 172
Db 81838 TACGCGGCCA 81847
```

```
RESULT 15
US-10-750-185-61749
; Sequence 61749, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
```

```
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61749
; LENGTH: 1485
; TYPE: DNA
; ORGANISM: Bovine 19866881469933
US-10-750-185-61749

Query Match 5.2%; Score 33.8; DB 6; Length 1485;
Best Local Similarity 50.3%; Pred. No. 2;
Matches 83; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

Qy 462 CTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGTGTCTTCTCACCCTGTGGCTGCT 521
Db 1291 CTCTGGTAAACAATGGAAAAATGATGTTCATCCAAAGACCATCTCCCTTTCTTACTGAA 1350
Qy 522 CATCGAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGAGCGAGCCCAAGAAAA 581
Db 1351 GCTCAGATAGAAAAATTTTACACCTTGGTAAACAGAGGCGCAGCTGGACAGAGAGAAAA 1410
Qy 582 CGCGTCTGACTACTTGTGCCATCCCATCTGAGAAACAGGAGAACTC 626
Db 1411 AGCCGAGTACAACATCATCACCATCACGGGCACTGACATGGGAACCC 1455
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Search completed: December 13, 2005, 14:42:59
Job time : 176.718 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
C 1	38.6	16.2	6242	3	US-09-949-016-16490	Sequence 16490, A	
C 2	37.8	15.9	14566	3	US-09-949-016-16765	Sequence 16765, A	
C 3	37.2	15.6	23640	3	US-09-949-016-13646	Sequence 13646, A	
C 4	37	15.5	767677	3	US-09-949-016-12147	Sequence 12147, A	
C 5	37	15.5	767677	3	US-09-949-016-17361	Sequence 17361, A	
C 6	36.2	15.2	7218	2	US-08-232-463-14	Sequence 14, Appl	
C 7	36.2	15.2	60276	3	US-09-949-016-15004	Sequence 15004, A	
C 8	36.2	15.2	60338	3	US-09-949-016-15694	Sequence 15694, A	
C 9	36	15.1	323820	3	US-09-949-016-14139	Sequence 14139, A	
C 10	35.8	15.0	71278	3	US-09-949-016-11851	Sequence 11851, A	
C 11	35.8	15.0	71278	3	US-09-949-016-17563	Sequence 17563, A	
C 12	35.8	15.0	168174	3	US-10-071-411A-63	Sequence 63, Appl	
C 13	35.8	15.0	168273	3	US-10-071-411A-2	Sequence 2, Appl	
C 14	35.4	14.9	601	3	US-09-949-016-74297	Sequence 74297, A	
C 15	35.4	14.9	601	3	US-09-949-016-74298	Sequence 74298, A	
C 16	35.4	14.9	30656	3	US-09-949-016-14613	Sequence 14613, A	
C 17	35.4	14.9	84761	3	US-09-949-016-11919	Sequence 11919, A	
C 18	35.4	14.8	84763	3	US-09-949-016-13914	Sequence 13914, A	
C 19	35.2	14.8	2482	3	US-10-104-047-520	Sequence 520, App	
C 20	35.2	14.8	18900	3	US-09-949-016-16989	Sequence 16989, A	
C 21	35.2	14.8	30000	3	US-10-007-010-10	Sequence 10, Appl	
C 22	35.2	14.8	53562	3	US-09-949-016-16286	Sequence 16286, A	
C 23	34.4	14.5	601	3	US-09-949-016-79198	Sequence 79198, A	
C 24	34.4	14.5	601	3	US-09-949-016-91783	Sequence 91783, A	

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16765
; LENGTH: 14566
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16765

Query Match      15.9%; Score 37.8; DB 3; Length 14566;
Best Local Similarity 60.0%; Pred. No. 0.037;
Matches 63; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 105 CTTCCCTTCATGCATCCATTGTTCTGTTTCATTCATTCATCATCCACCTGCCTCTG 164
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 528 CATCCCTCCATTCATCCATCCACCCATCCCTCATTCATTCATTCATTCATCCCTCCATTC 469
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 165 AGCTTTACCTCTGACTCCCTAACTCCATCAGACCTCTACGCACC 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 468 ATCATCCCTCCCTCATCCATCTATTCATCCATCACCACCCATC 424
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
US-09-949-016-13646
; Sequence 13646, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13646
; LENGTH: 23640
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)-(23640)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13646

Query Match      15.6%; Score 37.2; DB 3; Length 23640;
Best Local Similarity 65.9%; Pred. No. 0.073;
Matches 54; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 107 TCCCTTCATGCATCCATTGTTCTGTTTCATTCATTCATTCATCCACCTGCCTCTGAG 166
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7218 TCCATCCATGCACCCATCCATTCATTCATTCATTCATCCACCCATCTTCCACCTATCCATCCA 7277
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 167 CTTTCACCTCTGACTCCCTAAC 188
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7278 CTTATACTTCTACCTACCCATC 7299
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match      15.5%; Score 37; DB 3; Length 767677;
Best Local Similarity 60.4%; Pred. No. 0.41;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 109 CCTTCATGCATCCATTGTTCTGTTTCATTCATTCATTCATCCACCTGCCTCTGAGCT 168
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542579 CCTTCCTCATTCATCCATCCCTCCATTCATTCATTCATCCACCATCCATCTCTCT 542520
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 169 TTCACCTCTGACTCCCTAACTCCATCAGACCTCTACGCACC 209
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542519 TACATCCATCCACCCATCCATCTCTCTTCATCCATCCATC 542479
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match      15.5%; Score 37; DB 3; Length 767677;
Best Local Similarity 60.4%; Pred. No. 0.41;
Matches 61; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
```

```
QY 109 CCTTCATGCATCCATTGTTCTGTTTCATTTCATTCATCATCCACCTGCCTCTGAGCT 168
Db 542579 CCTTCCTCCATCCATCCATCCCTCCATCCATCCATCCATCCATCCATCCATCCAT 542520
QY 169 TTCACCTCTGACTCCCTAACTCAATCCATCAGACCTCTACGCACC 209
Db 542519 TACATCCATCACCACCCATCCATCCCTCTCTTCATCCATCCATC 542479

RESULT 6
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 15.2%; Score 36.2; DB 2; Length 7218;
Best Local Similarity 8.4%; Pred. No. 0.094;
Matches 17; Conservative 109; Mismatches 77; Indels 0; Gaps 0;

QY 20 GAGTGGCCCTGAACACCTGAGGAGCTGAGATCCCATCCATGTTTCAGCAATGTCAATGGCATCA 79
Db 1035 GAGCTTGGCTGCAGGTGCAGGAGCTTGCAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1094
QY 80 GGAGGGCGCCCAAGGAGCCCATCGCTTCCCTTCATCGCATCCATGTTCTGTTTCATTCAT 139
Db 1095 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1154
QY 140 TCATCCATACATCACCTGCTGAGCTTTCACCTCTGACTCCCTAACTCCATCCATCAGACC 199
Db 1155 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1214
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QY 200 TCTACGCACCATTAAGACTCTGCC 222
Db 1215 YYYYYYYYYYYYYYYYYYYYYYYY 1237

RESULT 7
US-09-949-016-15004
; Sequence 15004, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15004
; LENGTH: 60276
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(60276)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15004

Query Match 15.2%; Score 36.2; DB 3; Length 60276;
Best Local Similarity 57.5%; Pred. No. 0.25;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 111 TTCATGCATCCATTGTTCTGTTTCATTTCATTCATCCATCATCCATCCATCCATCCATCCAT 170
Db 11773 TCATCGATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 11832
QY 171 CACCTCTGACTCCCTAACTCCATCCATCAGACCTCTACGACCCATAAGACTCTGCCA 223
Db 11833 TCACCATCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 11885

RESULT 8
US-09-949-016-15694
; Sequence 15694, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15694
; LENGTH: 60338
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(60338)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15694

Query Match      15.2%; Score 36.2; DB 3; Length 60338;
Best Local Similarity 57.5%; Pred. No. 0.25;
Matches 65; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy 111 TTCATGATCCATTGTTCTGTTTCATTTCATCCATACATCCACCTGCGCTCTGAGCTTT 170
Db 11835 TCCATGATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCAT 11894
Qy 171 CACCTCTGACCTCCCTAACTCCATCAGACCTCTAGCGCACCAATAAGACTCTGCGCA 223
Db 11895 TCACCATCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 11947

RESULT 9
US-09-949-016-14139/c
; Sequence 14139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14139
; LENGTH: 323820
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(323820)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14139

Query Match      15.1%; Score 36; DB 3; Length 323820;
Best Local Similarity 70.6%; Pred. No. 0.62;
Matches 48; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 89 CCCAAGGCCCGCCATCGCTTCCCTTCATCCATCCATCCATCCATCCATCCATCCATCC 148
Db 88457 CTCAGGCGCCCTGTTCTCCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 88398
Qy 149 CATCCACC 156
Db 88397 CATCCAAC 88390

RESULT 10
US-09-949-016-11851/c
; Sequence 11851, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11851
; LENGTH: 71278
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(71278)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11851

Query Match      15.0%; Score 35.8; DB 3; Length 71278;
Best Local Similarity 56.3%; Pred. No. 0.36;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 105 CTTCCTTCATGCATCCATTGTTCTGTTTCATTTCATCCATACATCCACCTGCTCTG 164
Db 40115 CATCCATCCATCTATCCATCCATCTCTGTCTATATCTTCATCCATCCATCCATCC 40056
Qy 165 AGCTTTCACTCTGACTCCCTAACTCCATCCATCAGACCTCTACGCACCAATAAGACTCTG 223
Db 40055 ACCATCCACCCATCAATCCATCCATCCATCCATCCATCCATCCATCCATCTCATCTGTCA 39997

RESULT 11
US-09-949-016-17563/c
; Sequence 17563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17563
; LENGTH: 71278
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(71278)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17563

Query Match      15.0%; Score 35.8; DB 3; Length 71278;
Best Local Similarity 56.3%; Pred. No. 0.36;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 105 CTTCCTTCATGCATCCATTGTTCTGTTTCATTTCATCCATACATCCACCTGCTCTG 164
Db 40115 CATCCATCCATCTATCCATCCATCTCTGTCTATATCTTCATCCATCCATCCATCC 40056
Qy 165 AGCTTTCACTCTGACTCCCTAACTCCATCCATCAGACCTCTACGCACCAATAAGACTCTG 223
Db 40055 ACCATCCACCCATCAATCCATCCATCCATCCATCCATCCATCCATCCATCTCATCTGTCA 39997

RESULT 12
US-10-071-411A-63
; Sequence 63, Application US/10071411A
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Patent No. 6797475
GENERAL INFORMATION:
APPLICANT: Glenn Barnes
APPLICANT: Joanne Meyer
TITLE OF INVENTION: Detection of Polymorphisms in the Human
FILE REFERENCE: MRI-021
CURRENT APPLICATION NUMBER: US/10/071.411A
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,515
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/314,248
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 63
LENGTH: 168174
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(168174)
OTHER INFORMATION: n = A,T,C or G
US-10-071-411A-63

Query Match 15.0%; Score 35.8; DB 3; Length 168174;
Best Local Similarity 56.3%; Pred. No. 0.54;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 105 CTTCCTTCATGCATCCATGTTCTGTTTCATTCATCCATCCACCTGCTCTG 164
Db 12256 CATCCATCCATTCATCCATCCATCTCTGTTATCTTCCATCCACCATTC 12315
Qy 165 AGCTTTCACCTGACTCCCTCACTCCATCCATCCAGACTCTACGACCATAGACTCTGCA 223
Db 12316 ACCATCCACCATCAATCCATCCACCATCTATCCATCCATCCATCTCACTATCTGTCA 12374

RESULT 13
US-10-071-411A-2
Sequence 2, Application US/10071411A
Patent No. 6797475
GENERAL INFORMATION:
APPLICANT: Glenn Barnes
APPLICANT: Joanne Meyer
TITLE OF INVENTION: Detection of Polymorphisms in the Human
FILE REFERENCE: MRI-021
CURRENT APPLICATION NUMBER: US/10/071.411A
PRIOR FILING DATE: 2002-02-07
PRIOR APPLICATION NUMBER: 60/267,515
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: 60/314,248
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 168273
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(168273)
OTHER INFORMATION: n = A,T,C or G
US-10-071-411A-2

Query Match 15.0%; Score 35.8; DB 3; Length 168273;
Best Local Similarity 56.3%; Pred. No. 0.54;
Matches 67; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 105 CTTCCTTCATGCATCCATGTTCTGTTTCATTCATCCATCCACCTGCTCTG 164
Db 12256 CATCCATCCATTCATCCATCCATCTCTGTTATCTTCCATCCACCATTC 12315

Qy 165 AGCTTTCACCTGACTCCCTTAATCCTCAGACCTCTACGACCATAGACTCTGCA 223
Db 12316 ACCATCCACCATCAATCCATCCACCATCTATCCATCCATCTCACTATCTGTCA 12374

RESULT 14

US-09-949-016-74297
Sequence 74297, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74297
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-74297

Query Match 14.9%; Score 35.4; DB 3; Length 601;
Best Local Similarity 63.5%; Pred. No. 0.058;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 105 CTTCCTTCATGCATCCATGTTCTGTTTCATTCATCCATCCACCTGCTCTG 164
Db 217 CATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 276
Qy 165 AGCTTTCACCTGACTCCCTCACT 189
Db 277 AATTTTATTTCTCTCTCTCTCTCT 301

RESULT 15

US-09-949-016-74298
Sequence 74298, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74298
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-74298

Query Match 14.9%; Score 35.4; DB 3; Length 601;
Best Local Similarity 63.5%; Pred. No. 0.058;
Matches 54; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy	105	CTTCCTTCATGCATCCATTGTTCTGTTCATTTCATCCATACATCCACCTGCCTCTG	164
Db	158	CATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCACA	217
Qy	165	AGCTTTACCTCTGACTCCCTAACT	189
Db	218	AATTTTATTCTCTCTCTCTCT	242

Search completed: December 13, 2005, 07:35:20
Job time : 61.2062 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 07:13:57 ; Search time 271.784 Seconds
(without alignments)
7241.448 Million cell updates/sec

Title: US-09-977-579A-4_COPY_1024_1261

Perfect score: 238
Sequence: 1 aacaggagcagtgtgacatg.....tgccagaactgagaagccgg 238

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_Main.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	238	100.0	600	10	US-11-060-756-2816
2	238	100.0	600	10	US-11-060-756-2817
3	238	100.0	600	10	US-11-060-756-7088
4	238	100.0	600	10	US-11-060-756-7089
5	238	100.0	1261	3	US-09-977-579-4
6	238	100.0	1261	9	US-10-482-834A-22
7	216	90.8	4625	3	US-09-764-891-7659
8	87	36.6	495	4	US-09-925-065A-807954
9	87	36.6	502	4	US-09-925-065A-807996
10	86	36.1	495	4	US-09-925-065A-778585
11	40.6	17.1	599	4	US-09-925-065A-252659
12	40.6	17.1	2213000	5	US-10-174-014-12
13	40.6	17.1	233380	5	US-10-087-192-652
14	39.2	16.5	623	4	US-09-925-065A-944616
15	39.2	16.5	1702	4	US-09-925-065A-681163
16	39.2	16.5	1702	4	US-09-925-065A-681164
17	38.4	16.1	228	8	US-10-674-124A-21325
18	38	16.0	623	4	US-09-925-065A-917353
19	38	16.0	623	4	US-09-925-065A-944614
20	38	16.0	27079	6	US-10-034-650-55
21	38	16.0	38360	3	US-09-999-121-14
22	37.8	15.9	109	8	US-10-674-124A-4659
23	37.8	15.9	195	8	US-10-674-124A-4658

24	37.8	15.9	634	4	US-09-925-065A-499987	Sequence 499987,
25	37.8	15.9	634	4	US-09-925-065A-499988	Sequence 499988,
26	37.8	15.9	634	4	US-09-925-065A-499989	Sequence 499989,
27	37.8	15.9	634	4	US-09-925-065A-499990	Sequence 499990,
C 28	37.8	15.9	1091	5	US-10-027-632-30772	Sequence 30772, A
C 29	37.8	15.9	1091	6	US-10-027-632-30772	Sequence 30772, A
30	37.8	15.9	1327	5	US-10-027-632-215913	Sequence 215913,
31	37.8	15.9	1327	6	US-10-027-632-215913	Sequence 215913,
C 32	37.8	15.9	2750	4	US-09-925-065A-31066	Sequence 31066, A
C 33	37.8	15.9	2750	4	US-09-925-065A-31067	Sequence 31067, A
C 34	37.8	15.9	3768	3	US-09-969-708-464	Sequence 464, App
C 35	37.8	15.9	3768	3	US-09-954-531-164	Sequence 164, App
C 36	37.8	15.9	3768	3	US-09-954-531-373	Sequence 373, App
C 37	37.8	15.9	3768	3	US-09-960-706-1041	Sequence 1041, App
C 38	37.8	15.9	3768	3	US-09-873-319-689	Sequence 689, App
C 39	37.8	15.9	3768	9	US-10-843-641A-1231	Sequence 1231, Ap
C 40	37.8	15.9	3768	9	US-10-843-641A-1440	Sequence 1440, Ap
C 41	37.8	15.9	3768	9	US-10-843-641A-7935	Sequence 7935, Ap
C 42	37.8	15.9	3768	9	US-10-287-436A-642	Sequence 642, App
C 43	37.8	15.9	8222	9	US-10-486-319A-6	Sequence 6, Appli
C 44	37.8	15.9	8222	9	US-10-486-319A-42	Sequence 42, Appl
C 45	37.8	15.9	8222	9	US-10-486-319A-64	Sequence 64, Appl

ALIGNMENTS

RESULT 1

US-11-060-756-2816
; Sequence 2816, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2816
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-060-756-2816

Query Match	100.0%;	Score 238;	DB 10;	Length 600;
Best Local Similarity	100.0%;	Pred. No. 1e-68;		
Matches 238;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGGACTGGACATCCCATGTTTC	60	
Db	363	AACAGGAGCAGTGTGACATGAGTGGCTGAAACACCTGAGGGACTGGACATCCCATGTTTC	422	
Qy	61	AGCAATGTCATTAATGGCATCAGGAGGGGCGCCCAAGGGCCCATCGTTCCCTTCATGCATC	120	
Db	423	AGCAATGTCATTAATGGCATCAGGAGGGGCGCCCAAGGGCCCATCGTTCCCTTCATGCATC	482	
Qy	121	CATTGTTCTGTTTCATTTCATTCATCCATACATCCACCTGCTTCTGAGCTTTCACCTCTGAC	180	
Db	483	CATTGTTCTGTTTCATTTCATTCATCCATACATCCACCTGCTTCTGAGCTTTCACCTCTGAC	542	
Qy	181	TCCTTAATCCATCAGACCTCTAGCACCACATAGACTCTGCCAGAACTGAGAGCCCGG	238	
Db	543	TCCTTAATCCATCAGACCTCTAGCACCACATAGACTCTGCCAGAACTGAGAGCCCGG	600	

RESULT 2

US-11-060-756-2817
; Sequence 2817, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2817
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2817

Query Match 100.0%; Score 238; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 60
Db |
363 AACAGGAGCAGTGTGACATGAGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 422
QY 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 120
Db |
423 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 482
QY 121 CATTGTTCTGTTCATTCATTCATCATACATCCACCTGCGCTCTGAGCTTTCACCTCTGAC 180
Db |
483 CATTGTTCTGTTCATTCATTCATCATACATCCACCTGCGCTCTGAGCTTTCACCTCTGAC 542
QY 181 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCAGAACTGAGAGGCCGG 238
Db |
543 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCAGAACTGAGAGGCCGG 600

RESULT 3
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088

Query Match 100.0%; Score 238; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 60
Db |
363 AACAGGAGCAGTGTGACATGAGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 422
QY 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 120
Db |
423 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 482
QY 121 CATTGTTCTGTTCATTCATTCATCATACATCCACCTGCGCTCTGAGCTTTCACCTCTGAC 180
Db |
483 CATTGTTCTGTTCATTCATTCATCATACATCCACCTGCGCTCTGAGCTTTCACCTCTGAC 542
QY 181 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCAGAACTGAGAGGCCGG 238

Db 543 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCAGAACTGAGAGGCCGG 600
RESULT 4
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Query Match 100.0%; Score 238; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1e-68;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACAGGAGCAGTGTGACATGAGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 60
Db |
363 AACAGGAGCAGTGTGACATGAGTGGCTGAACACCTGAGGGACTGGACATCCCATGTTTC 422
QY 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 120
Db |
423 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGCTTCCCTTTCATGCATC 482
QY 121 CATTGTTCTGTTCATTCATTCATCATACATCCACCTGCGCTCTGAGCTTTCACCTCTGAC 180
Db |
483 CATTGTTCTGTTCATTCATTCATCATACATCCACCTGCGCTCTGAGCTTTCACCTCTGAC 542
QY 181 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCAGAACTGAGAGGCCGG 238
Db |
543 TCCCTAACTCCATCAGACCTCTACGCACCAATAGACTCTGCAGAACTGAGAGGCCGG 600

RESULT 5
US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated so
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match 100.0%; Score 238; DB 3; Length 1261;
Best Local Similarity 100.0%; Pred. No. 1.3e-66;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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RESULT 9
US-09-925-065A-807996/c
; Sequence 807996, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 807996
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-807996

Query Match      36.6%; Score 87; DB 4; Length 502;
Best Local Similarity 100.0%; Pred. No. 2e-18;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AGGTGGCTGAACACCTGAGGACTGGACATCCCATGTTGCAATGTCATGCGATCAG 80
Db 87 AGGTGGCTGAACACCTGAGGACTGGACATCCCATGTTGCAATGTCATGCGATCAG 28

Qy 81 GAGGGCGCCCCAAGGGCCCCATCGCTT 107
Db 27 GAGGGCGCCCCAAGGGCCCCATCGCTT 1

RESULT 10
US-09-925-065A-778585
; Sequence 778585, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 778585
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-778585

Query Match      36.1%; Score 86; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 4.2e-18;

Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 AGGTGGCTGAACACCTGAGGACTGGACATCCCATGTTGCAATGTCATGCGATCAG 80
Db 410 AGGTGGCTGAACACCTGAGGACTGGACATCCCATGTTTCCGCAATGTCATGCGATCAG 469

Qy 81 GAGGGCGCCCCAAGGGCCCCATCGCT 106
Db 470 GAGGGCGCCCCAAGGGCCCCATCGCT 495

RESULT 11
US-09-925-065A-252659
; Sequence 252659, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 252659
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-252659

Query Match      17.1%; Score 40.6; DB 4; Length 599;
Best Local Similarity 64.2%; Pred. No. 0.006;
Matches 61; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 105 CTTCCCTTCATGTCATTCATTTCTGTTTCATTCATCCATCCATCCCTGCTG 164
Db 328 CATACATTCATCCATTCATTTATTTATCCATCCATCCATCCATCCCTCTA 387

Qy 165 AGCTTTACCTCTGACTCCCTAACTCCATCCAGACC 199
Db 388 TCATTTATCCATCCATCCATCCATCCATCCGTC 422

RESULT 12
US-10-174-014-12
; Sequence 12, Application US/10174014
; Publication No. US20040005292A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Preier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMRT EXPRESSION
; FILE REFERENCE: PTS-0012
; CURRENT APPLICATION NUMBER: US/10/174,014
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 12
; LENGTH: 221000
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 77967
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; OTHER INFORMATION: unknown
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Matches 73; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 46 GGACATCCCATGTTTCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATGCG 105
Db 46047 GGAGTCCCATGCTGGGGAAGATTTCATTTCATTGGGAGTCCCATGCTGGGAGATCC 46106

Qy 106 TTCCTTCATGCATCCATTGTTCTTCATTTCATTCATCCATACATCCACCTGCTCTGA 165
Db 46107 ATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 46166

Qy 166 GCTTTCA 172
Db 46167 CTTATCA 46173
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RESULT 13
US-10-087-192-652
; Sequence 652, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 652
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; LENGTH: 233380
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(233380)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-652

Query Match
Best Local Similarity 17.1%; Score 40.6; DB 5; Length 233380;
Matches 73; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

Qy 46 GGACATCCCATGTTTCAGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCCATGCG 105
Db 55725 GGAGTCCCATGCTGGGGAAGATTTCATTTCATTGGGAGTCCCATGCTGGGAGATCC 55784

Qy 106 TTCCTTCATGCATCCATTGTTCTTCATTTCATTCATTCATCCATACATCCACCTGCTCTGA 165
Db 55785 ATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 55844

Qy 166 GCTTTCA 172
Db 55845 CTTATCA 55851
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RESULT 14
US-09-925-065A-944616
; Sequence 944616, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 944616
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-065A-944616
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Query Match
Best Local Similarity 16.5%; Score 39.2; DB 4; Length 623;
Matches 59; Conservative 1; Mismatches 34; Indels 0; Gaps 0;

Qy 97 CCCCATCGTTCCTTCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 156
Db 457 CCCCTTTCTTCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 516

Qy 157 TGCTCTGAGCTTTCACCTCTGACTCCCTAATC 190
Db 517 TATCTATCTAGCTACCGAGCTAGCTACCTRTATC 550
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RESULT 15
US-09-925-065A-681163/C
; Sequence 681163, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
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GenCore version 5.1.6
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(without alignments)
1386.561 Million cell updates/sec

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Perfect score: 238

Sequence: 1 aacaggagcagtgtgacatg.....tgccagaactgagaagccgg 238

Scoring table: IDENTITY NUC

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Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	238	100.0	1261	6	US-10-374-954-8
2	37.8	15.9	200628	7	US-11-121-086-62
3	37.2	15.6	126552	7	US-11-121-086-1
4	37.2	15.6	162173	7	US-11-121-086-72
5	36.6	15.4	181172	7	US-11-121-086-41
6	36	15.1	162537	7	US-11-121-086-59
7	34.6	14.5	169725	7	US-11-121-086-63
8	34.2	14.4	1408	6	US-10-750-185-50899
9	33.6	14.1	119160	7	US-11-121-086-12
10	32.8	13.8	150468	7	US-11-121-086-56
11	32.8	13.8	169495	7	US-11-121-086-61
12	32.8	13.8	193789	7	US-11-121-086-55
13	32.8	13.8	207908	7	US-11-121-086-21
14	32.8	13.8	212805	7	US-11-121-086-19
15	32.6	13.7	200628	7	US-11-121-086-62
16	32.4	13.6	148220	7	US-11-121-086-30
17	32.2	13.5	126552	7	US-11-121-086-1
18	32.2	13.5	191684	7	US-11-121-086-2
19	32	13.4	110847	7	US-11-121-086-11
20	32	13.4	119160	7	US-11-121-086-12
21	31.8	13.4	172111	7	US-11-121-086-28
22	31.4	13.2	1522	6	US-10-750-185-42215
23	31.4	13.2	1888	6	US-10-750-185-47114

24	31.4	13.2	149111	7	US-11-112-908-63	Sequence 63, Appl
25	31.4	13.2	157230	7	US-11-112-908-64	Sequence 64, Appl
c 26	31.2	13.1	175673	7	US-11-121-086-55	Sequence 55, Appl
c 27	31.2	13.1	218821	7	US-11-121-086-31	Sequence 31, Appl
c 28	31	13.0	150038	7	US-11-121-086-23	Sequence 23, Appl
c 29	30.8	12.9	1064	6	US-10-750-185-46647	Sequence 46647, A
c 30	30.8	12.9	1428	6	US-10-750-185-55230	Sequence 55230, A
c 31	30.6	12.9	2231	6	US-10-750-185-34561	Sequence 34561, A
c 32	30.4	12.8	110847	7	US-11-121-086-11	Sequence 11, Appl
c 33	30.4	12.8	110847	7	US-11-121-086-11	Sequence 11, Appl
c 34	30.4	12.8	157224	7	US-11-112-908-51	Sequence 51, Appl
c 35	30.4	12.8	170189	7	US-11-112-908-50	Sequence 50, Appl
c 36	30.4	12.8	235033	7	US-11-157-389-1	Sequence 1, Appl
c 37	30.4	12.8	237326	7	US-11-157-389-2	Sequence 2, Appl
c 38	30.2	12.7	1413	6	US-10-750-185-57194	Sequence 57194, A
c 39	30.2	12.7	176760	7	US-11-121-086-51	Sequence 51, Appl
c 40	30	12.6	2018	6	US-10-750-185-63929	Sequence 63929, A
c 41	30	12.6	319608	7	US-11-145-703-1	Sequence 1, Appl
c 42	29.8	12.5	600	6	US-10-750-185-1892	Sequence 1892, Ap
c 43	29.8	12.5	1172	6	US-10-750-185-40064	Sequence 40064, A
c 44	29.8	12.5	1487	6	US-10-750-185-38424	Sequence 38424, A
c 45	29.6	12.4	773	6	US-10-750-185-53566	Sequence 53566, A

ALIGNMENTS

RESULT 1
US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8

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Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACAGGAGCAGTGTGACATGAGTGGCGCTGAACACCTGAGGAGCTGGACATCCCATGTTTC 60
Db 1024 AACAGGAGCAGTGTGACATGAGTGGCGCTGAACACCTGAGGAGCTGGACATCCCATGTTTC 1083
Qy 61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGTTTCCCTTCATGCAATC 120
Db 1084 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGGCCCATCGTTTCCCTTCATGCAATC 1143
Qy 121 CATTTGTTCTGTTTCAATTCATTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 180
Db 1144 CATTTGTTCTGTTTCAATTCATTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1203
Qy 181 TCCTTAATCCATCAGACCTCTAGGACCATATAGACTCTGCAGAACTGAGAGCCCG 238
Db 1204 TCCTTAATCCATCAGACCTCTAGGACCATATAGACTCTGCAGAACTGAGAGCCCG 1261

; CURRENT APPLICATION NUMBER: US/11/121.086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
; LENGTH: 162537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-59

Query Match 15.1%; Score 36; DB 7; Length 162537;
Best Local Similarity 80.8%; Pred. No. 0.093;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy 105 CTTCCCTTCATGCATCCATGTTCTGTTTCATTCATTCATCCATACATCCACC 156
Db 65857 CTTCCATCCATTCATCCATTCATCTGTGTCATCCATCCATCCATCCATCCATC 65908

RESULT 7

US-11-121-086-63/c
; Sequence 63, Application US/11/121.086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 169725
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-63

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Best Local Similarity 59.8%; Pred. No. 0.26;
Matches 58; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
Qy 105 CTTCCCTTCATGCATCCATGTTCTGTTTCATTCATTCATCCATCCACCTCCCTGTG 164
Db 120076 CATCCACTCCATCCATCCATCCATTCATCCATCCATCCATCCATCCATCCATCCATCC 120017
Qy 165 AGCTTTCACCTCTGACTCCCTCACTCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 201
Db 120016 ATCCATTCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 119980

RESULT 8

US-10-750-185-50889
; Sequence 50889, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750.185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50889
; LENGTH: 1408
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-50889

Query Match 14.4%; Score 34.2; DB 6; Length 1408;
Best Local Similarity 71.4%; Pred. No. 0.057;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 107 TCCCTTCATCCATCCATGTTCTGTTTCATTCATTCATCCATACATCCACCTGCCTCTGAG 166
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Qy 167 CTT 169
Db 746 ATT 748

RESULT 9

US-11-121-086-12/c
; Sequence 12, Application US/11/121.086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 119160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-12

Query Match 14.1%; Score 33.6; DB 7; Length 119160;
Best Local Similarity 63.8%; Pred. No. 0.53;
Matches 51; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
Qy 102 TCCCTTCCTTCATGCATCCATGTTCTGTTTCATTCATTCATCCATCCACCTGCCT 161
Db 19829 TCTTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 19770
Qy 162 CTGAGCTTTCACCTCTGACT 181
Db 19769 CTATTCCTCTGTATGCCT 19750

RESULT 10

US-11-112-908-56
; Sequence 56, Application US/11/112.908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112.908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826

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GenCore version 5.1.6
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Title: US-09-977-579A-4

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 3	24	1.9	137949	3	US-09-949-016-12196, A
C 4	24	1.9	137956	3	US-09-949-016-17260, A
C 5	20	1.6	1491	3	US-09-902-540-6997, A
C 6	20	1.6	2517	3	US-09-712-363-4, A
C 7	20	1.6	4312	3	US-09-902-540-612, A
C 8	20	1.6	4403765	3	US-09-103-840A-2, A
C 9	20	1.6	4411529	3	US-09-103-840A-1, A
C 10	19	1.5	601	3	US-09-949-016-85015, A
C 11	19	1.5	601	3	US-09-949-016-85166, A
C 12	19	1.5	1626	2	US-08-381-433A-3, A
C 13	19	1.5	1626	3	US-09-799-978-17, A
C 14	19	1.5	1626	3	US-09-881-401-3, A
C 15	19	1.5	5895	3	US-09-902-540-792, A
C 16	19	1.5	109159	3	US-09-949-016-14169, A
C 17	19	1.5	109159	3	US-09-949-016-14170, A
C 18	18	1.4	344	3	US-09-157-177-128, A
C 19	18	1.4	344	3	US-09-541-210-128, A
C 20	18	1.4	466	3	US-09-280-116-14, A
C 21	18	1.4	570	3	US-09-621-976-1635, A
C 22	18	1.4	601	3	US-09-949-016-56070, A
C 23	18	1.4	601	3	US-09-949-016-122006, A
C 24	18	1.4	601	3	US-09-949-016-131295, A

ALIGNMENTS

RESULT 1

US-09-949-016-26733/c
; Sequence 26733, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26733
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26733

Query Match 1.9%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0

Qy 1156 CATTTCATTCATCATCCACC 1179

Db 472 CATTTCATTCATCATCCACC 449

RESULT 2

US-09-949-016-194175/c
; Sequence 194175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194175
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
;
Query Match          1.9%; Score 24; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1156 CATTTCATTCATCCATACATCCACC 1179
Db 472 CATTTCATTCATCCATACATCCACC 449

RESULT 3
US-09-949-016-12196
; Sequence 12196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12196
; LENGTH: 137949
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(137949)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12196

Query Match          1.9%; Score 24; DB 3; Length 137949;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1156 CATTTCATTCATCCATACATCCACC 1179
Db 130759 CATTTCATTCATCCATACATCCACC 130782

RESULT 4
US-09-949-016-17260
; Sequence 17260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17260
; LENGTH: 137956
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(137956)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17260

Query Match          1.9%; Score 24; DB 3; Length 137956;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1156 CATTTCATTCATCCATACATCCACC 1179
Db 130759 CATTTCATTCATCCATACATCCACC 130782

RESULT 5
US-09-902-540-6997
; Sequence 6997, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16925
; SEQ ID NO 6997
; LENGTH: 1491
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6997

Query Match          1.6%; Score 20; DB 3; Length 1491;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 665 GCAAGGACCTGCAGGACGTG 684
Db 1205 GCAAGGACCTGCAGGACGTG 1224

RESULT 6
US-09-712-363-4/c
; Sequence 4, Application US/09712363
; Patent No. 6892139
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
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; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; US-09-712-363-4

Query Match      1.6%; Score 20; DB 3; Length 2517;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      500 AGCTGCGCTGCATCTCTGTC 519
Db      82 AGCTGCGCTGCATCTCTGTC 63

RESULT 7
US-09-902-540-612/c
; Sequence 612, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 612
; LENGTH: 4312
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-612

Query Match      1.6%; Score 20; DB 3; Length 4312;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      665 GCAAGGACCTGCAGGACGTG 684
Db      291 GCAAGGACCTGCAGGACGTG 272

RESULT 8
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
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; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Query Match      1.6%; Score 20; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      500 AGCTGCGCTGCATCTCTGTC 519
Db      7383 AGCTGCGCTGCATCTCTGTC 7364

RESULT 9
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
; US-09-103-840A-1

Query Match      1.6%; Score 20; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      500 AGCTGCGCTGCATCTCTGTC 519
Db      7383 AGCTGCGCTGCATCTCTGTC 7364

RESULT 10
US-09-949-016-85015
; Sequence 85015, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85015
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-85015

Query Match          1.5%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 TGTTCATTCAATTCATCCAT 1170
Db 465 TGTTCATTCAATTCATCCAT 483

RESULT 11
US-09-949-016-85166
; Sequence 85166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85166
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-85166

Query Match          1.5%; Score 19; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1152 TGTTCATTCAATTCATCCAT 1170
Db 465 TGTTCATTCAATTCATCCAT 483

RESULT 12
US-08-381-433A-3
; Sequence 3, Application US/08381433A
; Patent No. 5786203
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy W.
; APPLICANT: Oltersdorff, Tilman
; APPLICANT: Liaw, Chen
; APPLICANT: Grigoriadis, Dimitri E.
; APPLICANT: DeSouza, Errol B.
; TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
; TITLE OF INVENTION: RECEPTORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/381,433A
; FILING DATE: 31-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 690068.401C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANDBERRY
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 216..1449
US-08-381-433A-3

Query Match          1.5%; Score 19; DB 2; Length 1626;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 CCGGGGTGGGGGGGAGGC 90
Db 95 CCGGGGTGGGGGGGAGGC 113

RESULT 13
US-09-799-978-17
; Sequence 17, Application US/09799978
; Patent No. 6670140
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert
; APPLICANT: Sheldon, Russell
; TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
; TITLE OF INVENTION: Function Using Corticotropin Releasing Factor Receptors
; FILE REFERENCE: 8448
; CURRENT APPLICATION NUMBER: US/09/799,978
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (216)..(1451)
US-09-799-978-17

Query Match          1.5%; Score 19; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 CCGGGGTGGGGGGGAGGC 90
Db 95 CCGGGGTGGGGGGGAGGC 113

RESULT 14
US-09-881-401-3
; Sequence 3, Application US/09881401
; Patent No. 6723841
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy W.
```

Oltersdorf, Tilman
Liaw, Chen
Grigoriadis, Dimitri E.
Chalmers, Derek T.
DeSouza, Erol B.
TITLE OF INVENTION: CORTICOTROPIN RELEASING FACTOR 2
RECEPTORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/881,401
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Christiansen, William T.
REGISTRATION NUMBER: 44,614
REFERENCE/DOCKET NUMBER: 690068.401C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 216..1449
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-881-401-3
Query Match 1.5%; Score 19; DB 3; Length 1626;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 72 CCGGGGTGGCGGGGAGGC 90
Db 95 CCGGGGTGGCGGGGAGGC 113
RESULT 15
US-09-902-540-792
Sequence 792, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 792
LENGTH: 5895
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-792

Query Match 1.5%; Score 19; DB 3; Length 5895;
Best Local Similarity 100.0%; Pred.No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Job time : 279 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2005, 14:31:47 ; Search time 1161 Seconds
(without alignments)
8981.641 Million cell updates/sec

Title: US-09-977-579A-4
Perfect score: 1261
Sequence: 1 cctctccttcgagctgagc.....tgccagaactgagaagccgg 1261

Scoring table: OLIGO NUC
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 - 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	600	47.6	600	10	US-11-060-756-2817
5	600	47.6	600	10	US-11-060-756-7088
6	600	47.6	600	10	US-11-060-756-7089
7	396	31.4	1195	9	US-10-450-763-22568
8	391	31.0	3531	9	US-10-450-763-22567
9	386	30.6	651	4	US-09-925-065A-513769
10	335	26.6	651	4	US-09-925-065A-513767
11	335	26.6	651	4	US-09-925-065A-513768
12	218	17.3	545	4	US-09-925-065A-774904
13	218	17.3	621	9	US-10-450-763-22566
14	216	17.1	4625	3	US-09-764-891-7659
15	91	7.2	407	7	US-10-276-774-718
16	87	6.9	496	4	US-09-925-065A-807954
17	87	6.9	502	4	US-09-925-065A-807996
18	86	6.8	495	4	US-09-925-065A-778585
19	44	3.5	53	9	US-10-491-192-5
20	44	3.5	60	9	US-10-491-192-6
21	42	3.3	642	4	US-09-925-065A-322798
22	42	3.3	642	4	US-09-925-065A-322799
23	38	3.0	645	5	US-10-029-191-21

24	38	3.0	2220	3	US-09-977-579-3	Sequence 3, Appli
25	38	3.0	2632	5	US-10-029-191-22	Sequence 22, Appli
26	38	3.0	3108	5	US-10-029-191-1	Sequence 1, Appli
27	33	2.6	574	3	US-09-764-891-1293	Sequence 1293, Ap
28	25	2.0	25	10	US-11-060-756-54798	Sequence 54798, A
29	25	2.0	25	10	US-11-060-756-54799	Sequence 54799, A
30	25	2.0	25	10	US-11-060-756-54800	Sequence 54800, A
31	25	2.0	25	10	US-11-060-756-54801	Sequence 54801, A
32	25	2.0	25	10	US-11-060-756-54802	Sequence 54802, A
33	25	2.0	25	10	US-11-060-756-54803	Sequence 54803, A
34	25	2.0	25	10	US-11-060-756-54804	Sequence 54804, A
35	25	2.0	25	10	US-11-060-756-54805	Sequence 54805, A
36	25	2.0	25	10	US-11-060-756-54806	Sequence 54806, A
37	25	2.0	25	10	US-11-060-756-54807	Sequence 54807, A
38	25	2.0	25	10	US-11-060-756-54808	Sequence 54808, A
39	25	2.0	25	10	US-11-060-756-54809	Sequence 54809, A
40	25	2.0	25	10	US-11-060-756-54810	Sequence 54810, A
41	25	2.0	25	10	US-11-060-756-54811	Sequence 54811, A
42	25	2.0	25	10	US-11-060-756-54812	Sequence 54812, A
43	25	2.0	25	10	US-11-060-756-54813	Sequence 54813, A
44	25	2.0	25	10	US-11-060-756-54814	Sequence 54814, A
45	25	2.0	25	10	US-11-060-756-54815	Sequence 54815, A

ALIGNMENTS

RESULT 1
US-09-977-579-4
; Sequence 4, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses t
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-977-579-4

Query Match	100.0%	Score 1261;	DB 3;	Length 1261;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1261;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCTCCCTCCGAGCTGAGCTTACCTCTGGCGCAACAGCAGCGAGGCGCGAGTGG	60	
Db	1	CCCTCCCTCCGAGCTGAGCTTACCTCTGGCGCAACAGCAGCGAGGCGCGAGTGG	60	
Qy	61	AAGCTGAGTTCGGGGTGGCGGGGAGGCGACTGTCCTGCTGAGCGCGCGCGAGA	120	
Db	61	AAGCTGAGTTCGGGGTGGCGGGGAGGCGACTGTCCTGCTGAGCGCGCGCGAGA	120	
Qy	121	GCGGCGCGAGCGGCTGATCGGCTCCCTGAACTGGGGAGGTCAGTGGGTCGCTTAG	180	
Db	121	GCGGCGCGAGCGGCTGATCGGCTCCCTGAACTGGGGAGGTCAGTGGGTCGCTTAG	180	
Qy	181	GGCCCAAGCCCGCCACCCCGGCTCCAAAAGCTCCAGAGGCTCCCGAGGACCGGTGCTCG	240	
Db	181	GGCCCAAGCCCGCCACCCCGGCTCCAAAAGCTCCAGAGGCTCCCGAGGACCGGTGCTCG	240	
Qy	241	GCCTTCCTTCGGTCAAGAAAGTGCCTCCCTGGGGGAGTTCGTCCTCCAAAGGTTCTCTCG	300	

Db 241 GCCCTTCTTCCGTCAGAAAGTCGCCCTTGGGGCAGTTCGTCCCAAAGGTTTCTCTCG 300
Qy 301 AAAGAACTCTGAGAGGCGCAGTCTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAACTCTGAGAGGCGCAGTCTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Qy 361 CGCAGAGCCCAAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGT 420
Db 361 CGCAGAGCCCAAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGT 420
Qy 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCTCGAGACGAGGCC 480
Db 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCTCGAGACGAGGCC 480
Qy 481 GTGACAGGCAACCCCATGAGCTGGCTGCATCTCTCTGCATGAGAGAGAGGTGGAG 540
Db 481 GTGACAGGCAACCCCATGAGCTGGCTGCATCTCTCTGCATGAGAGAGAGGTGGAG 540
Qy 541 GCCACACGGTGGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAC 600
Db 541 GCCACACGGTGGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAC 600
Qy 601 GAGTATCGGAATGGCCACAGAGGTGGAGGCCCTTTTACGGGCGCTCGAGTGAAT 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGGAGGCCCTTTTACGGGCGCTCGAGTGAAT 660
Qy 661 GGCAGCAAGGACCTCGAGAGGTGTCATCTCTGTGTCAACGTCACTCTGAAAGACTCT 720
Db 661 GGCAGCAAGGACCTCGAGAGGTGTCATCTCTGTGTCAACGTCACTCTGAAAGACTCT 720
Qy 721 GGCCTCTACACTGCAATGTGTCGGGAGTTTGAATTTGAGGGGCATCGGCCCTTTGTG 780
Db 721 GGCCTCTACACTGCAATGTGTCGGGAGTTTGAATTTGAGGGGCATCGGCCCTTTGTG 780
Qy 781 AAGACGACGGCTGATCCCCCTAAGAGTCAACGAGAGGTGGAGAGACTTTCACCTCT 840
Db 781 AAGACGACGGCTGATCCCCCTAAGAGTCAACGAGAGGTGGAGAGACTTTCACCTCT 840
Qy 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGTGTTCTTCTCACCTGTGCTCATC 900
Db 841 GTGGTCTCAGAAATCATGATGATACATCTTCTGTGTTCTTCTCACCTGTGCTCATC 900
Qy 901 GAGATGATATATGCTACAGAAAGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAACGG 960
Db 901 GAGATGATATATGCTACAGAAAGTCTCAAAAGCCGAGAGGCGAGCCCAAGAAACGG 960
Qy 961 TCTGACTACCTTGCCATCCCATCTGAGAACAGAGAACTCTGCGGTACCCAGTGGAGAA 1020
Db 961 TCTGACTACCTTGCCATCCCATCTGAGAACAGAGAACTCTGCGGTACCCAGTGGAGAA 1020
Qy 1021 TAGAACAGAGCAGTGTGATGAGTGGCTGTGAACACCTGAGGACCTGGACATCCCATG 1080
Db 1021 TAGAACAGAGCAGTGTGATGAGTGGCTGTGAACACCTGAGGACCTGGACATCCCATG 1080
Qy 1081 TTCAGCAATGTCAAATGGGATCAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTATGC 1140
Db 1081 TTCAGCAATGTCAAATGGGATCAGAGGGCGCCCAAGGGCCCATCGCTTCCCTTATGC 1140
Qy 1141 ATCCATTTGTTGTTTCATTTCATTATCCATATACATCCACCTGCTGTGAGCTTTCACCTCT 1200
Db 1141 ATCCATTTGTTGTTTCATTTCATTATCCATATACATCCACCTGCTGTGAGCTTTCACCTCT 1200
Qy 1201 GACTCCCTAACTCCATCAGACCTTACGACCAATAGACTCTGCGCAAGACTGAGAAGCG 1260
Db 1201 GACTCCCTAACTCCATCAGACCTTACGACCAATAGACTCTGCGCAAGACTGAGAAGCG 1260
Qy 1261 G 1261
Db 1261 G 1261

RESULT 2

US-10-482-834A-22

; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hilary Anny
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-482-834A-22

Query Match 96.0%; Score 1210; DB 9; Length 1261;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1260; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTCCCTTCGAGCTGAGCTTACCTTGGCGCAACGAGCGAGGCGGCGAGTGG 60
Db 1 CCCTCCCTTCGAGCTGAGCTTACCTTGGCGCAACGAGCGAGGCGGCGAGTGG 60
Qy 61 AAGTGGAGTTCGGGTGGCGGGAGGCGACTGTCCGTGGTCTGAGCCCGCGAGA 120
Db 61 AAGTGGAGTTCGGGTGGCGGGAGGCGACTGTCCGTGGTCTGAGCCCGCGAGA 120
Qy 121 GCGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGCTCAGTGGGGTGCCTAG 180
Db 121 GCGGCGCGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGCTCAGTGGGGTGCCTAG 180
Qy 181 GGGCCAAAGCCCCCAGCGGCTCCAAAGTCTCCAGGGCTCCCGAGGCAACGGTGTCTG 240
Db 181 GGGCCAAAGCCCCCAGCGGCTCCAAAGTCTCCAGGGCTCCCGAGGCAACGGTGTCTG 240
Qy 241 GCGCTTCTTCGGTCAAGAGTCCGCTCCGCGGCGAGTTCGTCCCAAGGGTTCCTCG 300
Db 241 GCGCTTCTTCGGTCAAGAGTCCGCTCCGCGGCGAGTTCGTCCCAAGGGTTCCTCG 300
Qy 301 AAAGAACTCTGAGAGGCGCAGTCTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Db 301 AAAGAACTCTGAGAGGCGCAGTCTCTTGACCGAGGGAATCTCTGTGTAGCCTTGGAGC 360
Qy 361 CGCAGAGCCCAAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGT 420
Db 361 CGCAGAGCCCAAGAGATGCGCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGT 420
Qy 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCTCGAGACGAGGCC 480
Db 421 ATCTACTGGGTGAGTGTCTGCTTCCCTGTGTGTGGAGTGCCTCTCGAGACGAGGCC 480
Qy 481 GTGACAGGCAACCCCATGAGCTGGCTGCATCTCTGCATGAGAGAGAGGTGGAG 540
Db 481 GTGACAGGCAACCCCATGAGCTGGCTGCATCTCTGCATGAGAGAGAGGTGGAG 540
Qy 541 GCCACACGGTGGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAC 600
Db 541 GCCACACGGTGGTGAATGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTAC 600
Qy 601 GAGTATCGGAATGGCCACAGAGGTGGAGGCCCTTTTACGGGCGCTCGAGTGAAT 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGGAGGCCCTTTTACGGGCGCTCGAGTGAAT 660
Qy 661 GGCAGCAAGGACCTGAGGAGCGTGTCCATCTACTGTGCTCAACGTCACTCTGAAAGACTCT 720

Db	661	GGCAGCAAGACCTGCGAGGACGTTGCTCATCACTGTCTCAACGTCACCTCTGGAACGACTCT	720
Qy	721	GGCTCTTACACCTGCAATGTTCCCGGAGTTTGGAGTTTTCAGGCGCATCGGCCCTTTGTG	780
Db	721	GGCTCTTACACCTGCAATGTTCCCGGAGTTTGGAGTTTTCAGGCGCATCGGCCCTTTGTG	780
Qy	781	AAGACGACGGGCTGATCCCCCTAAGAGTCAACGAGGAGCTGGAGAGACTTCACTCT	840
Db	781	AAGACGACGGGCTGATCCCCCTAAGAGTCACTGAGGAGCTGGAGAGACTTCACTCT	840
Qy	841	GTGGTCTCAGAAATCATGATGTACATCTTCTGTGTTCTCTCACTGCTGCTGCTCATC	900
Db	841	GTGGTCTCAGAAATCATGATGTACATCTTCTGTGTTCTCTCACTGCTGCTGCTCATC	900
Qy	901	GAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGGAGGAGCCCAAGAAAACGCG	960
Db	901	GAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGGAGGAGCCCAAGAAAACGCG	960
Qy	961	TCTGACTACCTTGCCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACAGTGGAGGAA	1020
Db	961	TCTGACTACCTTGCCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACAGTGGAGGAA	1020
Qy	1021	TAGAACAGGACGAGTGTACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATG	1080
Db	1021	TAGAACAGGACGAGTGTACATGAGTGGCTGAAACACCTGAGGAGCTGGACATCCCATG	1080
Qy	1081	TTGAGCAATGTCAATGTCATCAGAGGCGGCCCAAGGCGCCCATCGCTTCCCTTTCATGC	1140
Db	1081	TTGAGCAATGTCAATGTCATCAGAGGCGGCCCAAGGCGCCCATCGCTTCCCTTTCATGC	1140
Qy	1141	ATCCATTTGTTCTGTTTCATTCATTCATACATCCACCTGCTGAGCTTTTCACTCT	1200
Db	1141	ATCCATTTGTTCTGTTTCATTCATTCATACATCCACCTGCTGAGCTTTTCACTCT	1200
Qy	1201	GACTCCCTAACTCCATCAGACCTCTACGCCACCAAGAGTCTGCGAGAACTGAGAGCGG	1260
Db	1201	GACTCCCTAACTCCATCAGACCTCTACGCCACCAAGAGTCTGCGAGAACTGAGAGCGG	1260
Qy	1261	G 1261	
Db	1261	G 1261	

RESULT 3

US-11-060-756-2816

; Sequence 2816, Application US/11060756

; Publication No. US20050221354A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William Martin

; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; FILE OF INVENTION: Target Genes

; FILE REFERENCE: AM101083 (031896-042000)

; CURRENT APPLICATION NUMBER: US/11/060,756

; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2816

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-060-756-2816

Query Match 47.6%; Score 600; DB 10; Length 600;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	662	GCAGCAAGGACCTGCGAGGAGCTGTCCATCACTGTGCTCAACGTCACCTTGAACGACTCTG	721
Db	1	GCAGCAAGGACCTGCGAGGAGCTGTCCATCACTGTGCTCAACGTCACCTTGAACGACTCTG	60
Qy	722	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGGAGCGCATCGGCCCTTTGTGA	781

Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGGAGCGCATCGGCCCTTTGTGA	120
Qy	782	AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG	841
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG	180
Qy	842	TGCTCTCAGAAATCATGATGTATCTTCTTGGTCTTCTTCCATCCCTGTGCTGCTCATCG	901
Db	181	TGCTCTCAGAAATCATGATGTATCTTCTTGGTCTTCTTCCATCCCTGTGCTGCTCATCG	240
Qy	902	AGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGGAGGAGCCCAAGAAAACGCGT	961
Db	241	AGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAAGGAGGAGCCCAAGAAAACGCGT	300
Qy	962	CTGACTACCTTGGCCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACCACTGGAGGAAT	1021
Db	301	CTGACTACCTTGGCCATCCCATCTGAGAAACAAGAGAACTCTGCGGTACCACTGGAGGAAT	360
Qy	1022	AGAACAGGAGCAGTGTGACATGAGTGGCTGTGAACACCTGAGGAGCTGGACATCCCATGT	1081
Db	361	AGAACAGGAGCAGTGTGACATGAGTGGCTGTGAACACCTGAGGAGCTGGACATCCCATGT	420
Qy	1082	TCAGCAATGTCAATGTCATCAGAGGCGGCCCAAGGCGCCCATCGCTTCCCTTTCATGCA	1141
Db	421	TCAGCAATGTCAATGTCATCAGAGGCGGCCCAAGGCGCCCATCGCTTCCCTTTCATGCA	480
Qy	1142	TCCATTTGTTCTGTTTCATTCATTCATACATCCACCTGCTGCTTCCCTTTCATGCTCTG	1201
Db	481	TCCATTTGTTCTGTTTCATTCATTCATACATCCACCTGCTGCTTCCCTTTCATGCTCTG	540
Qy	1202	ACTCCCTAACTCCATCAGACCTCTAGCACCAATAAGACTCTGCCAGAACTGAGAGCGG	1261
Db	541	ACTCCCTAACTCCATCAGACCTCTAGCACCAATAAGACTCTGCCAGAACTGAGAGCGG	600

RESULT 4

US-11-060-756-2817

; Sequence 2817, Application US/11060756

; Publication No. US20050221354A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William Martin

; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; FILE OF INVENTION: Target Genes

; FILE REFERENCE: AM101083 (031896-042000)

; CURRENT APPLICATION NUMBER: US/11/060,756

; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2817

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-060-756-2817

Query Match 47.6%; Score 600; DB 10; Length 600;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	662	GCAGCAAGGACCTGCGAGGAGCTGTCCATCACTGTGCTCAACGTCACCTTGAACGACTCTG	721
Db	1	GCAGCAAGGACCTGCGAGGAGCTGTCCATCACTGTGCTCAACGTCACCTTGAACGACTCTG	60
Qy	722	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGGAGCGCATCGGCCCTTTGTGA	781
Db	61	GCCTCTACACCTGCAATGTGTCGCGGAGTTTGAGTTTGGAGCGCATCGGCCCTTTGTGA	120
Qy	782	AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG	841
Db	121	AGACGACGCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG	180
Qy	842	TGGTCTCAGAAATCATGATGTATCTTCTTGGTCTTCTTCCATCCCTGTGCTGCTCATCG	901

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Db 181 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCAACCTGTGGCTGCTCATCG 240
Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGAGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGAGCCCAAGAAACCGGT 300
Qy 962 CTGACTACTTTGCCATCCCATCTCAGAAACAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
Db 301 CTGACTACTTTGCCATCCCATCTCAGAAACAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 1141
Db 421 TCAGCAATGTCAATGGCATTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 480
Qy 1142 TCCATTGTTCTGTTCAATTCATTCATCCATCATCCACCTGCTGAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATTCATCCATCATCCACCTGCTGAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGAACTCTGCCAGAACTGAGAAGCGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGAACTCTGCCAGAACTGAGAAGCGG 600

RESULT 5
US-11-060-756-7088
; Sequence 7088, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7088
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7088
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Query Match 47.6%; Score 600; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 60

Qy 722 GCCTCTACCACTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACCACTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGCGCATCGGCCCTTTGTGA 120

Qy 782 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 841
Db 121 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 180

Qy 842 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCAACCTGTGGCTGCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCAACCTGTGGCTGCTCATCG 240

Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGAGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGAGCCCAAGAAACCGGT 300

Qy 962 CTGACTACTTTGCCATCCCATCTCAGAAACAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
```

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Db 301 CTGACTACTTTGCCATCCCATCTCAGAAACAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360
Qy 1022 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 420
Qy 1082 TCAGCAATGTCAATGGCATTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 1141
Db 421 TCAGCAATGTCAATGGCATTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 480
Qy 1142 TCCATTGTTCTGTTCAATTCATTCATCCATCATCCACCTGCTGAGCTTTCACCTCTG 1201
Db 481 TCCATTGTTCTGTTCAATTCATTCATCCATCATCCACCTGCTGAGCTTTCACCTCTG 540
Qy 1202 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGAACTCTGCCAGAACTGAGAAGCGG 1261
Db 541 ACTCCCTAACTCCATCAGACCTCTACGCACCATAGAACTCTGCCAGAACTGAGAAGCGG 600

RESULT 6
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089
```

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Query Match 47.6%; Score 600; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 600; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 721
Db 1 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTG 60

Qy 722 GCCTCTACCACTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGCGCATCGGCCCTTTGTGA 781
Db 61 GCCTCTACCACTGCAATGTGTCCCGGAGTTTGTAGTTTGTAGGCGCATCGGCCCTTTGTGA 120

Qy 782 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 841
Db 121 AGACGACCGGCTGATCCCTTAAGAGTCAACGAGGAGGCTGGAGAGACTTCACTCTG 180

Qy 842 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCAACCTGTGGCTGCTCATCG 901
Db 181 TGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCTCAACCTGTGGCTGCTCATCG 240

Qy 902 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGAGCCCAAGAAACCGGT 961
Db 241 AGATGATATATTGCTACAGAAAGTCTCAAAAGCCGAGAGGAGAGCCCAAGAAACCGGT 300

Qy 962 CTGACTACTTTGCCATCCCATCTCAGAAACAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 1021
Db 301 CTGACTACTTTGCCATCCCATCTCAGAAACAGGAGAACTCTGCGGTACCAAGTGGAGGAAT 360

Qy 1022 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 1081
Db 361 AGAACAGGAGCAGTGTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 420

Qy 1082 TCAGCAATGTCAATGGCATTGACATGAGTGGCCCTGGAACACCTGAGGAGCTGGACATCCCATGT 1141
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Matches 385; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 45 GCAGGGCGCGAGTGGAGTTCGGGGTGGCGGGAGCGCACTGTCGGTGGTG 104
Db 172 GCAGGGCGCGAGTGGAGTTCGGGGTGGCGGGAGCGCACTGTCGGTGGTG 231

Qy 105 CTGAGCGCGCGAGAGCGGGCGGGAGCGGCTGATCGGCTCCCTCAACTGGGGAGGTC 164
Db 232 CTGAGCGCGCGAGAGCGGGCGGGAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTC 291

Qy 165 CAGTGGGTCTCTAGGGCCCAAGCCCCACCGGCTCCAAAAGCTCCCAAGGCGCTCCC 224
Db 292 CAGTGGGTCTCTAGGGCCCAAGCCCCACCGGCTCCAAAAGCTCCCAAGGCGCTCCC 351

Qy 225 CAGGCACCGGTGCTCGGCCCTTCTTCGGTCAGAAAGTGCGCCCTGGGGCGAGTTCGTC 284
Db 352 CAGGCACCGGTGCTCGGCCCTTCTTCGGTCAGAAAGTGCGCCCTGGGGCGAGTTCGTC 411

Qy 285 CCAAAGGTTTCCTCGAAAGAACTCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTCT 344
Db 412 CCAAAGGTTTCCTCGAAAGAACTCTGAGAGGGCGCAGTCTTGACCGAGGGAATCTCTCT 471

Qy 345 GTGTAGCTTGGAGCGCGCCAGCCCCCAGAGATGCTGCCTTCAATAGATTGTTTCCCT 404
Db 472 GTGTAGCTTGGAGCGCGCCAGCCCCCAGAGATGCTGCCTTCAATAGATTGTTTCCCT 531

Qy 405 GCCTTCTCTCGTCTATCTACTGGG 430
Db 532 GCCTTCTCTCGTCTATCTACTGGG 557

RESULT 12

US-09-925-065A-774904
; Sequence 774904, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774904
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-774904

Query Match 17.3%; Score 218; DB 4; Length 545;
Best Local Similarity 100.0%; Pred. No. 6.8e-108;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 595 ATTTACGAGTATCGGAATGGCCACCAGGAGTGGAGAGCCCTTTCAGGGGGCGCTGCAG 654
Db 144 ATTTACGAGTATCGGAATGGCCACCAGGAGTGGAGAGCCCTTTCAGGGGGCGCTGCAG 203

Qy 655 TGGATGCGCAGCAAGGACCTGCGAGGACGTGCTCACTGTGCTCAACGTCACCTCTGAAC 714
Db 204 TGGATGCGCAGCAAGGACCTGCGAGGACGTGCTCACTGTGCTCAACGTCACCTCTGAAC 263

Qy 715 GACTCTGGCCTCTACACCTGCAATGTGTCCGGGAGTTTGAGTTTGAGGGCGCATCGGCC 774

Db 264 GACTCTGGCCTCTACACCTGCAATGTGTCCGGGAGTTTGAGTTTGAGGGCGCATCGGCC 323
Qy 775 TTTGTGAAGACGACGCGGCTGATCCCCCTTAAGAGTCAC 812
Db 324 TTTGTGAAGACGACGCGGCTGATCCCCCTTAAGAGTCAC 361

RESULT 13

US-10-450-763-22566
; Sequence 22566, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22566
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (40)..(282)
; OTHER INFORMATION: 95% homologous to Rattus norvegicus voltage-gated sodium
; channel beta-3 subunit, accession number AJ243395, Smith-Waterman
; OTHER INFORMATION: Score=397.

US-10-450-763-22566

Query Match 17.3%; Score 218; DB 9; Length 621;
Best Local Similarity 100.0%; Pred. No. 6.7e-108;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 595 ATTTACGAGTATCGGAATGGCCACCAGGAGTGGAGAGCCCTTTCAGGGGGCGCTGCAG 654
Db 58 ATTTACGAGTATCGGAATGGCCACCAGGAGTGGAGAGCCCTTTCAGGGGGCGCTGCAG 117

Qy 655 TGGATGCGCAGCAAGGACCTGCGAGGACGTGCTCACTGTGCTCAACGTCACCTCTGAAC 714
Db 118 TGGATGCGCAGCAAGGACCTGCGAGGACGTGCTCACTGTGCTCAACGTCACCTCTGAAC 177

Qy 715 GACTCTGGCCTCTACACCTGCAATGTGTCCGGGAGTTTGAGTTTGAGGGCGCATCGGCC 774
Db 178 GACTCTGGCCTCTACACCTGCAATGTGTCCGGGAGTTTGAGTTTGAGGGCGCATCGGCC 237

Qy 775 TTTGTGAAGACGACGCGGCTGATCCCCCTTAAGAGTCAC 812
Db 238 TTTGTGAAGACGACGCGGCTGATCCCCCTTAAGAGTCAC 275

RESULT 14

US-09-764-891-7659
; Sequence 7659, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 7659

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; LENGTH: 4625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-891-7659

Query Match      17.1%; Score 216; DB 3; Length 4625;
Best Local Similarity 100.0%; Pred. No. 7.3e-107;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1044 AGTGGCCCTGAACACCTGAGGACTGGACATCCCATGTTTACAGCAATGTCATATGGCATCAG 1103
DB 33 AGTGGCCCTGAACACCTGAGGACTGGACATCCCATGTTTACAGCAATGTCATATGGCATCAG 92

QY 1104 GAGGCGGCCCAAGGGCCCCCATCGCTTCCCTTTCATGATCCATGTTTCTGTTTCATT 1163
DB 93 GAGGCGGCCCAAGGGCCCCCATCGCTTCCCTTTCATGATCCATGTTTCTGTTTCATT 152

QY 1164 CATCATATACATCCACCTGCTCTGAGCTTTTACCTCTGACTCCCTAACTCCATCAGACCT 1223
DB 153 CATCATATACATCCACCTGCTCTGAGCTTTTACCTCTGACTCCCTAACTCCATCAGACCT 212

QY 1224 CTAGCACCATAAGACTCTGCCAGAACTGAGAAGCC 1259
DB 213 CTAGCACCATAAGACTCTGCCAGAACTGAGAAGCC 248
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RESULT 15
US-10-276-774-718/c
; Sequence 718, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 718
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-774-718
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Query Match      7.2%; Score 91; DB 7; Length 407;
Best Local Similarity 99.3%; Pred. No. 1.6e-38;
Matches 141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 820 GCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGTCTTC 879
DB 230 GCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTTCTGTCTTC 171

QY 880 CTCACCTGTGGCTGCTCATCGAGATGATATATTCCTACAGAAAGGTCTCAAAAGCCGAA 939
DB 170 CTCACCTGTGGCTGCTCATCGAGATGATATATTCCTACAGAAAGGTCTCAAAAGCCGAA 111

QY 940 GAGGCGGCCCAAGAAACGCGT 961
DB 110 GAGGCGGCCCAAGAAACGCGT 89
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Job time : 1164 secs

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OM nucleic - nucleic search, using sw model

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Title: US-09-977-579A-4

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1261	100.0	1261	6	US-10-374-954-8
2	50	4.0	880	6	US-10-750-185-44336
3	19	1.5	19	8	US-11-101-244-1098655
4	19	1.5	19	8	US-11-101-244-1098661
5	19	1.5	19	8	US-11-101-244-1098665
6	19	1.5	19	8	US-11-101-244-1098671
7	19	1.5	19	8	US-11-101-244-1098679
8	19	1.5	19	8	US-11-101-244-1098688
9	19	1.5	19	8	US-11-101-244-1098692
10	19	1.5	19	8	US-11-101-244-1098695
11	19	1.5	19	8	US-11-101-244-1098711
12	19	1.5	19	8	US-11-101-244-1098717
13	19	1.5	19	8	US-11-101-244-1098723
14	19	1.5	19	8	US-11-101-244-1098724
15	19	1.5	19	8	US-11-101-244-1098725
16	19	1.5	19	8	US-11-101-244-1098733
17	19	1.5	19	8	US-11-101-244-1098734
18	19	1.5	19	8	US-11-101-244-1098740
19	19	1.5	19	8	US-11-101-244-1098746
20	19	1.5	19	8	US-11-101-244-1098748
21	19	1.5	19	8	US-11-101-244-1098655
22	19	1.5	19	9	US-11-083-784-1098661
23	19	1.5	19	9	US-11-083-784-1098665

ALIGNMENTS

RESULT 1
US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8

Query Match	100.0%	Score 1261;	DB 6;	Length 1261;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1261;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCCTCCCTCCGAGCTGAGCTTACCTCGGGCGGCAACGAGGAGGCGGCGAGTGG	60	
Db	1	CCCTCCCTCCGAGCTGAGCTTACCTCGGGCGGCAACGAGGAGGCGGCGAGTGG	60	
Qy	61	AAGCTGAGTTCGCGGGTGGCGGGAGGCGGCTGCTCCGTGCTGCTGAGCGCCGCGAGA	120	
Db	61	AAGCTGAGTTCGCGGGTGGCGGGAGGCGGCTGCTCCGTGCTGCTGAGCGCCGCGAGA	120	
Qy	121	CGCGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCACATGGGGTGCCTTAG	180	
Db	121	CGCGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGGGAGGTCACATGGGGTGCCTTAG	180	
Qy	181	GGCCCAAGCCCCCACCACCGGCTCCAAAGTCCCAAGGCTCCCAAGGCTCCCAAGGCTCC	240	
Db	181	GGCCCAAGCCCCCACCACCGGCTCCAAAGTCCCAAGGCTCCCAAGGCTCCCAAGGCTCC	240	

Qy 241 GCCCTTCCTTCGGTCAGAAAGTCGCCCTCGGGGCGAGTTTCGTCCCAAGAGGTTTCCTCG 300
Db 241 GCCCTTCCTTCGGTCAGAAAGTCGCCCTCGGGGCGAGTTTCGTCCCAAGAGGTTTCCTCG 300
Qy 301 AAAGAACTGAGAGGGCGCAGTCTTGACCCAGAGGAATCTCTGTGTAGGCTTGGAGC 360
Db 301 AAAGAACTGAGAGGGCGCAGTCTTGACCCAGAGGAATCTCTGTGTAGGCTTGGAGC 360
Qy 361 CGCCAGGCCCAAGAGATGCGCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGTCTT 420
Db 361 CGCCAGGCCCAAGAGATGCGCTTCAATAGATTGTTTCCCTCGGCTTCTCTCGTCTT 420
Qy 421 ATCTACTGGGTCACTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Db 421 ATCTACTGGGTCACTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGCGAGGCC 480
Qy 481 GTGAGGGCAACCCCATGAAGCTGGCTGCATCTCTGTCATGAAGAGAGAGGAGTGGAG 540
Db 481 GTGAGGGCAACCCCATGAAGCTGGCTGCATCTCTGTCATGAAGAGAGAGGAGTGGAG 540
Qy 541 GCCACCAAGTGGTGAATGTTCTACAGGCCCGAGGCGGTAAAGATTTCTTATTAT 600
Db 541 GCCACCAAGTGGTGAATGTTCTACAGGCCCGAGGCGGTAAAGATTTCTTATTAT 600
Qy 601 GAGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAA 660
Db 601 GAGTATCGGAATGGCCACAGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAA 660
Qy 661 GGCAGCAAGACCTGCGAGGAGTGTCCATCTGTGTCTCAACGTCATCTGAAAGACTCT 720
Db 661 GGCAGCAAGACCTGCGAGGAGTGTCCATCTGTGTCTCAACGTCATCTGAAAGACTCT 720
Qy 721 GGCCTCTACCTGCAATGTCCTCGGAGTTTCAGTTTGAAGGCGCATCGGCCCTTTGTG 780
Db 721 GGCCTCTACCTGCAATGTCCTCGGAGTTTCAGTTTGAAGGCGCATCGGCCCTTTGTG 780
Qy 781 AAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGTGGAGAGACTTCACCTCT 840
Db 781 AAGACGACGCGGCTGATCCCCCTAAGAGTCAACGAGGAGGTGGAGAGACTTCACCTCT 840
Qy 841 GTGCTCTCAGAAATCATGATGATACATCTTCTGTCTTCCTCACCTGTGCTGCTCATC 900
Db 841 GTGCTCTCAGAAATCATGATGATACATCTTCTGTCTTCCTCACCTGTGCTGCTCATC 900
Qy 901 GAGATGATATATGCTACAGAAAGTCTCAAAAGCGAGAGGAGGAGCCCAAGAAACGCG 960
Db 901 GAGATGATATATGCTACAGAAAGTCTCAAAAGCGAGAGGAGGAGCCCAAGAAACGCG 960
Qy 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
Db 961 TCTGACTACCTTGCCATCCCATCTGAGAAACAGAGAACTCTGCGGTACCAAGTGGAGAA 1020
Qy 1021 TAGAACAGGACAGTGTGACATGAGTGGCTGTAACACCTGAGGAGCTGGACATCCCATG 1080
Db 1021 TAGAACAGGACAGTGTGACATGAGTGGCTGTAACACCTGAGGAGCTGGACATCCCATG 1080
Qy 1081 TTCAGCATCTCAATGGCATCAGAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Db 1081 TTCAGCATCTCAATGGCATCAGAGGGGCGCCCAAGGGCCCATCGCTTCCCTTCATGC 1140
Qy 1141 ATCCATTTGTTGTTTCATTTCATTCATATCATATCATATCCATCTGCTTGTAGCTTTT 1200
Db 1141 ATCCATTTGTTGTTTCATTTCATTCATATCATATCCATCTGCTTGTAGCTTTT 1200
Qy 1201 GACTCCCTTAATCCATCAGACTCTTACGCAACATTAAGACTCTGCGAGAACTGAGAGCG 1260
Db 1201 GACTCCCTTAATCCATCAGACTCTTACGCAACATTAAGACTCTGCGAGAACTGAGAGCG 1260
Qy 1261 G 1261
Db 1261 G 1261

RESULT 2
US-10-750-185-44336
; Sequence 44336, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44336
; LENGTH: 880
; TYPE: DNA
; ORGANISM: Bovine 1986680898198
US-10-750-185-44336
Query Match 4.0%; Score 50; DB 6; Length 880;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 820 GCTGGAGGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTCT 869
Db 443 GCTGGAGGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGATCATCTCT 492
RESULT 3
US-11-101-244-1098655
; Sequence 1098655, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098655
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098655
Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
Qy 903 GATCATATATGCTTACAGA 921
Db 1 GAUCAUAUUGCUACAGA 19
RESULT 4
US-11-101-244-1098661

; Sequence 1098661, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098661
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098661

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 331 GAGGAATCTCTGTGTGA 349
|||||:|:|:|:|:|:|:
Db 1 GAGGAAAUUCUCUGUGUA 19

RESULT 5
US-11-101-244-1098665
; Sequence 1098665, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098665
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098665

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.9;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 711 GAACGACTCTGGCTCTAC 729
|||||:|:|:|:|:|:|:
Db 1 GAACGACUCUGGCCUCUAC 19

RESULT 6
US-11-101-244-1098671
; Sequence 1098671, Application US/11101244

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098671
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098671

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 845 TCTCAGAAATCATGATGTA 863
|||||:|:|:|:|:|:|:
Db 1 UCUCAGAAAUCAUGUGUA 19

RESULT 7
US-11-101-244-1098679
; Sequence 1098679, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
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; SOFTWARE: Proprietary
; SEQ ID NO 1098679
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098679

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.9;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;
QY 579 CGGTAAGATTTCTTTATT 597
|||||:|:|:|:|:|:|:
Db 1 CGGTAAGAUUUCUUAU 19

RESULT 8
US-11-101-244-1098688
; Sequence 1098688, Application US/11101244
; Publication No. US20050246794A1

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098688
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098688

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 57.9%; Pred. No. 2.9;
Matches 11; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1153 GTTCATTCATTCATCCATA 1171
|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 GUCAUUAUUAUUAUUAU 19

RESULT 9

US-11-101-244-1098692
; Sequence 1098692, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098692
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098692

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 937 GAAGAGGAGCCCAAGAAA 955
|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 GAAGAGGAGCCCAAGAAA 19

RESULT 10

US-11-101-244-1098695
; Sequence 1098695, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098695
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098695

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 68.4%; Pred. No. 2.9;
Matches 13; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 901 GAGATGATATATTCCTACA 919
|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 GAGAUAUAUAUUAUUAU 19

RESULT 11

US-11-101-244-1098711
; Sequence 1098711, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098711
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098711

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 73.7%; Pred. No. 2.9;
Matches 14; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 763 GCGCATCGGCCCTTTGTGA 781
|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 GCGCAUCGCGCCCUUGUGA 19

RESULT 12

US-11-101-244-1098717
; Sequence 1098717, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098717
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098717

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 936 CGAAGAGGCGACCCCAAGAA 954
|||||
Db 1 CGAAGAGGCGACCCCAAGAA 19

RESULT 13

US-11-101-244-1098723
; Sequence 1098723, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098723
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098723

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 GACATGAGTGGCCTGAAC 1056
|||||
Db 1 GACAUGAGGUGCCUGAAC 19

RESULT 14

US-11-101-244-1098724
; Sequence 1098724, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098724
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098724

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.9;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1023 GAACAGAGCAGTGTGACA 1041
|||||
Db 1 GAACAGAGCAGUGUGACA 19

RESULT 15

US-11-101-244-1098725
; Sequence 1098725, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1098725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1098725

Query Match 1.5%; Score 19; DB 8; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.9;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 993 GGAGAACTCTGCGGTACCA 1011
|||||
Db 1 GGAGAACUCUGCGGUACCA 19

Search completed: December 13, 2005, 17:21:37
Job time : 214 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 13, 2005, 14:47:42 ; Search time 193 Seconds
(without alignments)
1980.185 Million cell updates/sec

Title: US-09-977-579A-2

Perfect score: 1124

Sequence: 1 MPANRLPLASLVLVYWS.....SDYLAIPSENKENSAPVVEE 215

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7

Database :

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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	470	41.8	617	3	US-09-949-016-2369 Sequence 2369, Ap
2	165.5	14.7	11174	3	US-09-949-016-14111 Sequence 14111, A
3	165.5	14.7	30337	3	US-09-949-016-13053 Sequence 13053, A
4	147	13.1	1342	3	US-09-949-016-787 Sequence 787, App
5	147	13.1	1371	3	US-09-991-181-388 Sequence 388, App
6	147	13.1	1371	3	US-09-990-444-388 Sequence 388, App
7	147	13.1	1371	3	US-09-997-333-388 Sequence 388, App
8	147	13.1	1371	3	US-09-992-598-388 Sequence 388, App
9	147	13.1	1708	3	US-09-949-016-4948 Sequence 4948, Ap

10	131	11.7	1121	3	US-09-949-016-5103 Sequence 5103, Ap
11	131	11.7	1151	3	US-09-430-503-1 Sequence 1, Appli
12	131	11.7	1151	3	US-09-430-503-3 Sequence 3, Appli
13	131	11.7	1151	3	US-09-430-503-5 Sequence 5, Appli
14	131	11.7	1151	3	US-09-430-503-7 Sequence 7, Appli
15	131	11.7	1151	3	US-10-095-131A-1 Sequence 1, Appli
16	131	11.7	1151	3	US-10-095-131A-3 Sequence 3, Appli
17	131	11.7	1151	3	US-10-095-131A-5 Sequence 5, Appli
18	131	11.7	1151	3	US-10-095-131A-7 Sequence 7, Appli
19	131	11.7	1777	3	US-10-012-231A-363 Sequence 363, App
20	131	11.7	1777	3	US-10-015-389A-363 Sequence 363, App
21	131	11.7	1777	3	US-10-006-768A-363 Sequence 363, App
22	131	11.7	1777	3	US-10-015-671A-363 Sequence 363, App
23	131	11.7	1777	3	US-10-015-393A-363 Sequence 363, App
24	131	11.7	1777	3	US-10-011-833A-363 Sequence 363, App
25	131	11.7	1777	3	US-10-006-041A-363 Sequence 363, App
26	131	11.7	1777	3	US-10-012-064A-363 Sequence 363, App
27	129	11.5	600	3	US-09-430-503-43 Sequence 43, Appl
28	129	11.5	600	3	US-09-430-503-47 Sequence 47, Appl
29	129	11.5	600	3	US-10-095-131A-43 Sequence 43, Appl
30	129	11.5	600	3	US-10-095-131A-47 Sequence 47, Appl
31	127	11.3	600	3	US-09-430-503-41 Sequence 41, Appl
32	127	11.3	600	3	US-09-430-503-45 Sequence 45, Appl
33	127	11.3	600	3	US-10-095-131A-41 Sequence 41, Appl
34	127	11.3	600	3	US-10-095-131A-45 Sequence 45, Appl
35	127	11.3	752	3	US-09-430-503-17 Sequence 17, Appl
36	127	11.3	752	3	US-09-430-503-19 Sequence 19, Appl
37	127	11.3	752	3	US-09-430-503-21 Sequence 21, Appl
38	127	11.3	752	3	US-09-430-503-23 Sequence 23, Appl
39	127	11.3	752	3	US-10-095-131A-17 Sequence 17, Appl
40	127	11.3	752	3	US-10-095-131A-19 Sequence 19, Appl
41	127	11.3	752	3	US-10-095-131A-21 Sequence 21, Appl
42	127	11.3	752	3	US-10-095-131A-23 Sequence 23, Appl
43	125	11.1	1073	3	US-09-430-503-25 Sequence 25, Appl
44	125	11.1	1073	3	US-09-430-503-27 Sequence 27, Appl
45	125	11.1	1073	3	US-09-430-503-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-2369
; Sequence 2369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2369
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2369

Alignment Scores:
Pred. No.: 2.91e-50 Length: 617
Score: 470.00 Matches: 101
Percent Similarity: 66.16% Conservative: 30
Best Local Similarity: 51.01% Mismatches: 59
Query Match: 41.81% Indels: 8
DB: 3 Gaps: 5

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US-09-977-579A-2 (1-215) x US-09-949-016-2369 (1-617)
Qy 26 CysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCys 45
Db 21 TGCCTGGAGGTGAGTCTGGAGACCGGCGGTGTATGGGATGACCTTCAAAATTCCTTGC 80
Qy 46 IleSerCysMetLysArgGluGluValGluAlaThrValValGluTyrPheTyrArg 65
Db 81 ATCTCTCCAGAGCGCGGAGGAGACCAACGCTGAGACCTTCCAGGAGTGCCTTCGC 140
Qy 66 ProGluGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db 141 CAGAAGGCGACTGAGGAGTTGTCAAGATCTCGGCTATGAGATGAGGTGTTGCAGTG 200
Qy 85 GluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAsp 99
Db 201 GAGGAGGATGAGCGCTTCGAGGCGCGGTGTGTGGAATGGCAGCGCGGGCACCAGAC 260
Qy 100 LeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThr 119
Db 261 CTGAGGATCTGTCTATCTTATCACCNAATGTACCTTACCACTCGGGCAGTACGAG 320
Qy 120 CysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArg 139
Db 321 TGCCACGCTACCGCTCTCTTCTTGAAATACGAGACCAACACGCGTCTGCAAG 380
Qy 140 LeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGlu 159
Db 381 AAGATCCACATTGAGGTAGTGACAAAGCCCAACAGAGACATGGCATCCTGCTCTGAG 440
Qy 160 IleMetMetTyrIleLeuLeuValPheLeuThrLeuTyrLeuLeuGluMetIleTyr 179
Db 441 ATCATGATGATGCTCATGTGTGTGTGTTGACCATATGCTCTGTCGTCGAGATGATTAC 500
Qy 180 CysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyr 198
Db 501 TGCTACAGAAGATCGCTGCCGCCAGCGAGACTGCTGCACAGGAGATGCTCGGAATAC 560
Qy 199 LeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db 561 CTGGCCATCACCCTCTGAAAGCAAGAGAACTGCACGGCGCTCCAGGTGGCCGAA 614

RESULT 2
US-09-949-016-14111
; Sequence 14111, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14111
; LENGTH: 11174
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(11174)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14111
Alignment Scores: 1.21e-09 Length: 11174
Pred. No.:

US-09-977-579A-2 (1-215) x US-09-949-016-14111 (1-11174)
Qy 67 GluGlyGlyLysAspPheLeuIleTyrGlu-TyrArgAsnGlyHisGlnGluValGluSe 86
Db 8220 GAAGGAGGTATTCATTTCATTTAGGACCGTGTGAGGCGCTCCAG-AATGACACAGATGT 8273
Qy 86 rProPheGlnGlyArgLeu-----GlnTrp-----AsnGlySerLysAs 99
Db 8274 ACTTGCCCAAGGTCACACAGCTGGCCAGTGGCAGAGCCAGCCTTTGAACCTGAGCCTTCT 8333
Qy 99 pLeuGlnAspValSerIle-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
Db 8334 GGTTGCAGAGTACGGCTTTTAGGACCGTGTGAGGCGCTCCAG-AATGACACAGATGT 8392
Qy 117 uTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArg-----132
Db 8393 GGCTCGAGTTACACAGGAGGAGGTGTGAGGTCACCCACAGGCGCTACCCAGGCT 8452
Qy 133 -----ProPheValLysThrThrArgLeuIleProLeu-----143
Db 8453 GGGTATTATTAATACAGTGCATACACAGCCCGGAGGTTGAGCCACTCATCCAAGC 8512
Qy 143 -----143
Db 8513 TCACACAGCAAGCTCACAGCACACTCAGGCTGTCTATGCAGCGCTGGGCTTACCCCTTAACC 8572
Qy 144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db 8573 CTGCTCGGCCCTGCACGCCAACAGAGACATGGCATCCTCGTGTCTGAGATCATGATGA 8632
Qy 163 rIleLeuLeuValPheLeuThrLeuTyrLeuLeuGluMetIleTyrCysTyrArgLy 183
Db 8633 TGTGCTCATTTGTGTGTGTGTTGACCATATGCTCTGTCGTCGAGAGATGATTACTGCTACAAG 8692
Qy 183 sValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db 8693 GATCGCTCGCCACCGAGAGACTGCTGCACAGGAGATGCG 8732

RESULT 3
US-09-949-016-13053
; Sequence 13053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13053
; LENGTH: 30337
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(30337)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13053
```


, APPLICANT: Gurney, Austin L.
, APPLICANT: Kljavin, Ivar J.
, APPLICANT: Napier, Mary A.
, APPLICANT: Pan, James
, APPLICANT: Paoni, Nicholas F.
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, APPLICANT: Stewart, Timothy A.
, APPLICANT: Tunas, Daniel
, APPLICANT: Watanabe, Colin K.
, APPLICANT: Williams, P. Mickey
, APPLICANT: Wood, William I.
, APPLICANT: Zhang, Zemin
, TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
, FILE OF INVENTION: Acids Encoding the Same
, FILE REFERENCE: P2730P1C3
, CURRENT APPLICATION NUMBER: US/09/991,181
, CURRENT FILING DATE: 2001-11-16
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, PRIOR APPLICATION NUMBER: 60/090540

[illegible]

; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 1 22e-08 Length: 1371
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-990-444-388 (1-1371)

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Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuAryCysIle 46
Db 223 -----CTGAGGCTGTAAATGGGACAGATGCTCGGTTTAAATGCACCT 264
Qy 47 SerCysMetLysArgGluValGluAlaThrThrValValGluTyrPheTyrArgPro 66
Db 265 TTCTCCAGCTTTGCCCTGTGGGTGATGCTCTACAGTGACC---TGGAAATTTTGTCTCT 321
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Db 322 CTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTCCAACCCATG 381
Qy 85 GluSerProGlnGlyArgLeuGlnTyrAsnGlySerLysAspLeuGlnAspValSer 104
Db 382 AGTGGCGGTTTAAAGGACCGGTTCTCTGGGATGGGAATCCTGAGCGGTACGATGCTCTCC 441
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Db 442 ATCTCTCTGGAACTGCGATGTCGACGACAAATGGGACATACACCTCCAGGTGAAGAAC 501
Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
Db 502 -----CCACCTGAT 510
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Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaAalaGlnGlu 193
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Qy 214 GluGlu 215
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RESULT 7

US-09-977-333-388
; Sequence 388, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C27
; CURRENT APPLICATION NUMBER: US/09/997,333
; CURRENT FILING DATE: 2001-11-15
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.: 1.22e-08 Length: 1371
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
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Query Match: 13.08% Indels: 50
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-997-333-388 (1-1371)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db 181 CTTTGGCTATAGCAGCT--GTGAAATTATACCTCCCGGTG----- 222
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Db 223 -----CTGGAGGCTGTTAATGGACAGATGCTCGGTTAAATGCACT 264
Qy 47 SerCysMetLysArgGluValGluAlaThrThrValValGluTyrPheTyrArgPro 66
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Qy 85 GluSerProPheGlnGlyArgLeuGlnTyrAsnGlySerLysAspLeuGlnAspValSer 104
Db 382 AGTGGCGGTTTAGGACCGGCTCTTGGATGGGAATCCTGACCGGTACGATGCCTCC 441
Qy 105 IleThrValLeuAenValThrLeuAsnAspSerGlyLeuTyrThrCysAenValSerArg 124
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US-09-992-598-388

; Sequence 388, Application US/09992598

; Patent No. 6956108

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

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; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P27301C20

; CURRENT APPLICATION NUMBER: US/09/992,598

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

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; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16


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Qy 214 GluGlu 215
Db 730 GAGAAA 735

RESULT 9
US-09-949-016-4948
; Sequence 4948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4948
; LENGTH: 1708
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4948

Alignment Scores:
Pred. No.: 1.69e-08 Length: 1708
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-949-016-4948 (1-1708)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCys 26
Db 225 CTTTGGCCTATAGCAGCT--GTGGAATTTATACCTCCCGGGG----- 266
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 267 -----CTGAGGCTGTTAATGGGACAGATGCTCGTTAAATGCACT 308
Qy 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgPro 66
Db 309 TTCTCCAGCTTGGCCCTGCGGTGATGCTTAACAGTGACC---TGGAAATTTTCGTCT 365
Qy 67 ---GluGlyGly---LysAspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluVal 84
Db 366 CTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCAATAGATGCTTCCACCCATG 425
Qy 85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
Db 426 AGTGGCGGTTTAGGACCGGTCTTGGATGGGAATCTGACCGGTAGCATGCTCC 485
Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArg 124
Db 486 ATCTCTCTCGAAACTTCAGTTCGACGACAAATGGGACATACACCTCCAGGTGAAGAAC 545
Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
Db 546 -----CCACCTGAT 554
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db 555 GTTGATGGGTGATAGGGAGATCCGGCTCAGCGTCTGTCGACACTGTACGCTTCTCTGAG 614
Qy 160 IleMetMetTyrIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
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Db 615 ATCCACTTCTGCTCTGGCCATTGGCTCTGCTGTGCACTGATGATCATATAGTAATT 674
Qy 174 LeuIleGluMetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaGlnGlu 193
Db 675 GTAGTGGTCTCTTCCAGCATTTACCGGAAAAAGCGATGGCCGAAAGAGCT----- 725
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 726 -----CATAAAGTGGTGAGATAAAATCAAAAGAGGAAGGCTCAACCAA 773
Qy 214 GluGlu 215
Db 774 GAGAAA 779

RESULT 10
US-09-949-016-5103
; Sequence 5103, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5103
; LENGTH: 1121
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5103

Alignment Scores:
Pred. No.: 9.82e-07 Length: 1121
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-949-016-5103 (1-1121)

Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAGAAATCTTCGTGGCAAAATGGTACACAGGAAGCTGACCTGC--- 306
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAGTCTACTAGTACGCTGGGGTGTGACCTCAGTCTCTCTGAGC 357
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCACGCCAGAGGGGCGGACACTACTGTGCTGCTTTTCCACTACTCCCAGGCGCAAGTG 417
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 418 TACCTTGGGAATTTATCCACCATTTAAAGACAGATCAGCTGGGCTGGAGACCTTGACAAG 477
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 478 AAAGATGCATCAATCAACATAGAAATATGACGTTTATACACAAATGGCACCCTATCTGT 537
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 538 GATGTCAAAAC----- 549
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Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 550 ---CCTCTGCATCGTTGTCCAGCTGGACACATTAGGCTCTATGCTGTAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGGCTGTTTCCAGTTGGTAGTGGGCGATAGTTACTGTGCTGCTCTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTCTGCTCATCAGCATGATTCTGCTCTCTATAGAGGAAAAAACTCTAAACGG 726
Qy 184 -----ValSerLysAlaGluGluAlaAlaGlnGlu 193
Db 727 GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTTGTAAGAGTCTGCCCTTCTGGATCTCACACAGGCCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852
RESULT 11
US-09-430-503-1
; Sequence 1, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-1
Alignment Scores:
Pred. No.: 1.02e-06 Length: 1151
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9
US-09-977-579A-2 (1-215) x US-09-430-503-1 (1-1151)
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAGAAATCTTCTGGCAATGTGTACACAGGGGAAGCTGACCTGC--- 306
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValcIuTrpPhe 63
Db 307 -----AAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCCTGGAGC 357
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCCAGCCAGAGGGGGCCGACACTACTGTGCTGCTTTTTCCTACTCTCCAAAGGGCAAGTG 417
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
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Db 418 TACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGCTGGAGACCTTGTACAAG 477
Qy 101 GluAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuThrCys 120
Db 478 AAAGATGCATCAATCAACATAGAAAATATACAGTTTATACACAATGGCACCCTATATCTGT 537
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 538 GATGTCAAAAAC----- 549
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 550 ---CCTCTGCATCGTTGTCCAGCTGGACACATTAGGCTCTATGCTGTAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGGCTGTTTCCAGTTGGTAGTGGGCGATAGTTACTGTGCTGCTCTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTCTGCTCATCAGCATGATTCTGCTCTCTATAGAGGAAAAAACTCTAAACGG 726
Qy 184 -----ValSerLysAlaGluGluAlaAlaGlnGlu 193
Db 727 GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTTGTAAGAGTCTGCCCTTCTGGATCTCACACAGGCCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852
RESULT 12
US-09-430-503-3
; Sequence 3, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-3
Alignment Scores:
Pred. No.: 1.02e-06 Length: 1151
Score: 131.00 Matches: 51
Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
DB: 3 Gaps: 9
US-09-977-579A-2 (1-215) x US-09-430-503-3 (1-1151)
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAGAAATCTTCTGGCAATGTGTACACAGGGGAAGCTGACCTGC--- 306
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```
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAAGTCTACTAGTACGACTGGCGGTTGACCTCAGTCTCCTCGAGC 357
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCGAGCAGAGGGGGCGACACTACTGTGTGCGTTTTTCCACTACTCCCAAGGCAAGTG 417
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 418 TACCTTGGGAATTATCCACCATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG 477
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 478 AAAGATGCATCAATCAACATAGAAAATATGAGTTTATACAAATGGCACCCTATATCTGT 537
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 538 GATGTCAAAAAC----- 549
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 550 ---CCTCTGCATCGTTGTCACCGCTGGACACATTAGGCTCTATGTCGTAGAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGCTGTGTTCCAGTTTGGTAGTGGTGGCATAGTTACTGCTGTGCTTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTGCTCATCAGCATGATTCTGGCTGTGGTGGCATAGTTACTGCTGTGCTTAGGT 726
Qy 184 -----ValSerLysAlaGluGluAlaAalaGlnGlu 193
Db 727 GATTACACTGGCTGAGTACATCAGAGAGTTTGTACACAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTTGTAAGAGTCTGCTCTCTGATCTCACCAGGGCCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852

RESULT 13
US-09-430-503-5
; Sequence 5, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-5

Alignment Scores:
Pred. No.: 1.02e-06 Length: 1151
Score: 131.00 Matches: 51
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Percent Similarity: 37.39% Conservative: 32
Best Local Similarity: 22.97% Mismatches: 81
Query Match: 11.65% Indels: 58
Db: 3 Gaps: 9

US-09-977-579A-2 (1-215) x US-09-430-503-5 (1-1151)
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 250 GTATATACGCCAAAGAAAATCTTCTGGTCAAAATGGTACACAAAGGGAAGCTGACCTGC--- 306
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 307 -----AAGTTCAAGTCTACTAGTACGACTGGCGGTTGACCTCAGTCTCCTCGAGC 357
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln 82
Db 358 TTCGAGCAGAGGGGGCGACACTACTGTGTGCGTTTTTCCACTACTCCCAAGGCAAGTG 417
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 418 TACCTTGGGAATTATCCACCATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG 477
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 478 AAAGATGCATCAATCAACATAGAAAATATGAGTTTATACAAATGGCACCCTATATCTGT 537
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 538 GATGTCAAAAAC----- 549
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu--- 159
Db 550 ---CCTCTGCATCGTTGTCACCGCTGGACACATTAGGCTCTATGTCGTAGAGAAAAGAG 606
Qy 160 -----IleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 607 AATTGCTGTGTTCCAGTTTGGTAGTGGTGGCATAGTTACTGCTGTGCTTAGGT 666
Qy 171 LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 667 CTCACCTGCTCATCAGCATGATTCTGGCTGTGGTGGCATAGTTACTGATCTCACCAGGGCCCA 846
Qy 184 -----ValSerLysAlaGluGluAlaAalaGlnGlu 193
Db 727 GATTACACTGGCTGAGTACATCAGAGAGTTTGTACACAGTTAAGCAGGCTCTCGGAAG 786
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 787 TCCCCCTCCGACACTGAGGGCTTTGTAAGAGTCTGCTCTCTGATCTCACCAGGGCCCA 846
Qy 210 AlaVal 211
Db 847 GTCATA 852

RESULT 14
US-09-430-503-7
; Sequence 7, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (P2R) AND
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: Gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-09-430-503-7

Alignment Scores:

Pred. No.:	1.02e-06	Length:	1151
Score:	131.00	Matches:	51
Percent Similarity:	37.39%	Conservative:	32
Best Local Similarity:	22.97%	Mismatches:	81
Query Match:	11.65%	Indels:	58
DB:	3	Gaps:	9

US-09-977-579A-2 (1-215) x US-09-430-503-7 (1-1151)

Qy	27	ValGluValProSerGluThrGluAlaValGlnGlyAsnPrometLysLeuArgCysIle	46
Db	250	GTATATACGCCCAAGAAATCTTCGTGGCAATGGTACACAAAGGGAAGCTGACCTGC---	306
Qy	47	SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe	63
Db	307	-----AAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCCTGGAGC	357
Qy	64	TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln	82
Db	358	TTCCAGCCAGAGGGCGGCACACTACTGTGCTGCTTTTCCACTACTCCAAAGGCAAGTG	417
Qy	83	GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	418	TACCTTGGGAATATCCACCAATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG	477
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	478	AAAGATGATCAATCAATCAACATAGAAAATATGCAGTTTATACAAATGGCACCTATATCTGT	537
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	538	GATGTCAAAAC-----	549
Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu---	159
Db	550	---CCTCCTGACATCGTTGCCAGCTCGACACATAGGCTCTATGTCGTAGAAAAAGAG	606
Qy	160	-----IleMetMetTyrIleLeuLeuValPheLeuThr	170
Db	607	AATTTGCTGTGTTTCCAGTTTGGTAGTGGTGGGCATAGTTACTGCTGTGCTCTAGGT	666
Qy	171	LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys-----	183
Db	667	CTCACTGCTCATCAGCATGATTCTGGCTGCTCTATAGAGGAACTCTAAACGG	726
Qy	184	-----ValSerLysAlaGluGluAlaGlnGlu	193
Db	727	GATTACACTGGCTGAGTACATCAGAGTGTGTCACCAAGTTAAGCAAGCTCTCGGAAG	786
Qy	194	AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer	209
Db	787	TCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCTTCTGGATCTCACCAGGGGCCA	846
Qy	210	AlaVal 211	
Db	847	GTCA 852	

RESULT 15

US-10-095-131A-1
; Sequence 1, Application US/10095131A
; Patent No. 6939952
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME

; FILE REFERENCE: Attorney Docket No. 6939952 1242-11/2/2
; CURRENT APPLICATION NUMBER: US/10/095,131A
; CURRENT FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)..(1151)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (133)..(939)
US-10-095-131A-1

Alignment Scores:

Pred. No.:	1.02e-06	Length:	1151
Score:	131.00	Matches:	51
Percent Similarity:	37.39%	Conservative:	32
Best Local Similarity:	22.97%	Mismatches:	81
Query Match:	11.65%	Indels:	58
DB:	3	Gaps:	9

US-09-977-579A-2 (1-215) x US-10-095-131A-1 (1-1151)

Qy	27	ValGluValProSerGluThrGluAlaValGlnGlyAsnPrometLysLeuArgCysIle	46
Db	250	GTATATACGCCCAAGAAATCTTCGTGGCAATGGTACACAAAGGGAAGCTGACCTGC---	306
Qy	47	SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe	63
Db	307	-----AAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCCTGGAGC	357
Qy	64	TyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGln	82
Db	358	TTCCAGCCAGAGGGCGGCACACTACTGTGCTGCTTTTCCACTACTCCAAAGGCAAGTG	417
Qy	83	GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu	100
Db	418	TACCTTGGGAATATCCACCAATTTAAAGACAGAAATCAGCTGGCTGGAGACCTTGACAAG	477
Qy	101	GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
Db	478	AAAGATGATCAATCAACATAGAAAATATGCAGTTTATACAAATGGCACCTATATCTGT	537
Qy	121	AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu	140
Db	538	GATGTCAAAAC-----	549
Qy	141	IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGlu---	159
Db	550	---CCTCCTGACATCGTTGCCAGCTCGACACATAGGCTCTATGTCGTAGAAAAAGAG	606
Qy	160	-----IleMetMetTyrIleLeuLeuValPheLeuThr	170
Db	607	AATTTGCTGTGTTTCCAGTTTGGTAGTGGTGGGCATAGTTACTGCTGTGCTCTAGGT	666
Qy	171	LeuTrpLeuLeuIleGluMetIleTyrCys-----TyrArgLys-----	183
Db	667	CTCACTGCTCATCAGCATGATTCTGGCTGCTCTATAGAGGAACTCTAAACGG	726
Qy	184	-----ValSerLysAlaGluGluAlaGlnGlu	193
Db	727	GATTACACTGGCTGAGTACATCAGAGTGTGTCACCAAGTTAAGCAAGCTCTCGGAAG	786
Qy	194	AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer	209
Db	787	TCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCTTCTGGATCTCACCAGGGGCCA	846
Qy	210	AlaVal 211	

Db 847 GTCATA 852

Search completed: December 13, 2005, 17:25:13
Job time : 210 secs

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US-09-977-579A-2 (1-215) x US-09-977-579-4 (1-1261)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATATCTACGTGGTCACT 435

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTTCGAGACGGAGCGGTGCGAGGGCAACCCC 495

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAAGCTGCCTGCATCTCTCGATGAAGAGAGAGGAGGTGGAGGCCACACCGTGGTG 555

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGCCCGAGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGGC 615

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACGAGGAGGTGGAGAGGCCCTTTTCAGGGCGCCTGCAGTGGATGGCAGCAAGACCTG 675

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 735

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCCTGGGAGTTTGAGTTTGAGCGGCATCGGCCCTTTGTGAAGACACGCGGCTG 795

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAGAGTCAACGAGAGCTGGAGGAGCTTCACTCTGTGGTCTCAGAAATC 855

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTTCTGCTTCTCCCTGCTGGCTGCTCATCGAGATGATATATGC 915

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrIleuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCGGAGAGCAGCCCAAGAAACCGGCTCTGACTACCTTGCC 975

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGGAGGAA 1020

RESULT 2

; Sequence 22, Application US/10482834A
; Publication No. US20050074764A1
; GENERAL INFORMATION:
; APPLICANT: Mulley, John Charles
; APPLICANT: Harkin, Louise Anne
; APPLICANT: Dibbens, Michelle
; APPLICANT: Wallace, Robyn
; APPLICANT: Phillips, Hilary Ann
; APPLICANT: Heron, Sara Elizabeth
; APPLICANT: Berkovic, Samuel Frank
; APPLICANT: Scheffer, Ingrid Eileen
; APPLICANT: Bionomics Limited
; TITLE OF INVENTION: MUTATIONS IN ION CHANNELS
; FILE REFERENCE: 1386/17
; CURRENT APPLICATION NUMBER: US/10/482,834A
; CURRENT FILING DATE: 2004-01-02
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-834A-22

Alignment Scores:
Pred. No.: 3-53e-143 Length: 1261
Score: 1124.00 Matches: 215
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-482-834A-22 (1-1261)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCCTGCCTTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATATCTACGTGGTCACT 435

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTTCGAGACGGAGCGGTGCGAGGGCAACCCC 495

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 496 ATGAAGCTGCCTGCATCTCTCGATGAAGAGAGAGGAGGTGGAGGCCACACCGTGGTG 555

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGCCCGAGGCGGTAAAGATTTCCTTATTACGAGTATCGGAATGGC 615

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACGAGGAGGTGGAGAGGCCCTTTTCAGGGCGCCTGCAGTGGATGGCAGCAAGACCTG 675

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCTCTACACCTGC 735

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCCTGGGAGTTTGAGTTTGAGCGGCATCGGCCCTTTGTGAAGACACGCGGCTG 795

Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 796 ATCCCTTAAGAGTCAACGAGAGCTGGAGGAGCTTCACTCTGTGGTCTCAGAAATC 855

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuIleGluMetIleTyrCys 180
Db 856 ATGATGTACATCTTCTGCTTCTCCCTGCTGGCTGCTCATCGAGATGATATATGC 915

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrIleuAla 200
Db 916 TACAGAAAGGTCTCAAAAGCGGAGAGCAGCCCAAGAAACCGGCTCTGACTACCTTGCC 975

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGAACAGGAGAACTCTGCGGTACCACTGGAGGAA 1020

RESULT 3

US-10-029-191-21
; Sequence 21, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 21
; LENGTH: 645

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; TYPE: DNA
; ORGANISM: Rattus sp.
; US-10-029-191-21

Alignment Scores:
Pred. No.: 5 09e-141 Length: 645
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-21 (1-645)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 1 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTCATCTACTGGTGCAGA 60
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 61 GTCTGCTTCCCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTCATCTACTGGTGCAGA 60
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 121 ATGAGCTGAGGTGCATCTCTCGCATGAGAGGAGGAGGTGGAGGCCACCATCTGGTG 180
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 181 GAGTGGTTCTACAGGCTTACAGGCGGTAAAGATTTCCTATATATAGTATCGGAATGCG 240
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 241 CACGAGGAAGTGGAGAGCCCTTCCAAAGGCGGTCTGCAGTGGAAATGGGAGCAAGACCTG 300
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 301 CAGACGTATCCATCACTACTGACTCAATGTCACTTTGAATGACTCTGGCCCTCTACACATGC 360
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 361 AATGTGTCCAGGAGTTGGAATTCGAGGCACACAGGCGCTTTTGTGAAGACACAGAGACTG 420
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 421 ATACCTTTGGCAGTCACTGAAGAGCGGAGAGACTTCACCTCCGCTGGTCTCGGAATC 480
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 481 ATGATGTACATCTCTGGTCTTCCCTACCTTGTGGCTGTTTATTTGAGATGATCTATTGC 540
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 541 TACAGAAAGTCTCTAAGCCGAGAGAGGAGGAGCAGAGAAATGCGTCTGACTACCTTGCT 600
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 601 ATCCCTTCAGAGAACAGGAGAACTCTGTGTACCTGTGGAGGAA 645

RESULT 4
US-09-977-579-3
; Sequence 3, Application US/09977579
; Publication No. US20040248240A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge University Technical Services
; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sod
; TITLE OF INVENTION: channel
; TITLE OF INVENTION: channel
; FILE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses b
; FILE REFERENCE: 674558-2001
; CURRENT APPLICATION NUMBER: US/09/977,579
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: PCT/EP00/01783
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60,129,473
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; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: rat
; US-09-977-579-3

Alignment Scores:
Pred. No.: 3 45e-140 Length: 2220
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 3 Gaps: 0

US-09-977-579A-2 (1-215) x US-09-977-579-3 (1-2220)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 363 ATGCTGCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTCATCTACTGGTGCAGA 422
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 423 GTCTGCTTCCCTTCAACAGATTGCTTCCCTAGCTTCTTAGTGTCTCATCTACTGGTGCAGA 482
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValVal 60
Db 483 ATGAGCTGAGGTGCATCTCTCGCATGAGAGGAGGAGGTGGAGGCCACCATCTGGTG 542
Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 543 GAGTGGTTCTACAGGCTTACAGGCGGTAAAGATTTCCTATATATAGTATCGGAATGCG 602
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 603 CACGAGGAAGTGGAGAGCCCTTCCAAAGGCGGTCTGCAGTGGAAATGGGAGCAAGACCTG 662
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 663 CAGAGCATCACTACTGACTCAATGTCACTTTGAATGACTCTGGCCCTCTACACATGC 722
Qy 121 AsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 723 AATGTGTCCAGGAGTTCGAAATTCGAGGCACACAGGCGCTTTTGTGAAGACACAGAGACTG 782
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIle 160
Db 783 ATACCTTTGGCAGTCACTGAAGAGCGGAGAGACTTCACCTCCGCTGGTCTCGGAATC 842
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGluMetIleTyrCys 180
Db 843 ATGATGTACATCTCTGGTCTTCCCTACCTTGTGGCTGTTTATTTGAGATGATCTATTGC 902
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 903 TACAGAAAGTCTCTAAGCCGAGAGAGGAGGAGCAGAGAAATGCGTCTGACTACCTTGCT 962
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 963 ATCCCTTCAGAGAACAGGAGAACTCTGTGTGTACCTGTGGAGGAA 1007

RESULT 5
US-10-029-191-22
; Sequence 22, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
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; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2632
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-22

Alignment Scores:
Pred. No.: 4,49e-140 Length: 2632
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-22 (1-2632)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCCTGCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTACTGGGTGAGA 137

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGTGGAAGTCCCTCGGAGACAGAGCGGTGCAGGGCAATCCC 197

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTGCATGAAGAGGAGGAGGTGGAGGCCACCATCTGTGTG 257

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 CAGTGGTTCTACAGCCCTGAGGCGGTAAAGATTTCTTATATAGTATCGGAATGGC 317

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACCAGGAAGTGGAGAGCCCTTCCAGGCGGTCTGCAGTGGAAATGGGAGCAAGACCTG 377

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGCTACTCAATGTCACTTTGAATGACTCTGGCTCTACACATGC 437

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 438 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCAACGAGACTG 497

Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValSerGluIle 160
Db 498 ATACCTTTGCGAGTCACTGAAGAGCGGAGAAAGACTTCACTCCGTGGTCTCGGAATC 557

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCTCCTGCTTCTCCTACCTTGTGGCTGTTTATTGAGATGATCTATTGC 617

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGGTCTCTAAGGCCGAGAGGACACAGGAAATGCGTCTGACTACCTTGTCT 677

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTCAGAGAACAGAGAACTCTGTGGTACCCTGTGGAGGAA 722

RESULT 6
US-10-029-191-1
; Sequence 1, Application US/10029191
; Publication No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
```

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; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147.00XX/SUI
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3108
; TYPE: DNA
; ORGANISM: Rattus sp.
US-10-029-191-1

Alignment Scores:
Pred. No.: 5,81e-140 Length: 3108
Score: 1105.00 Matches: 211
Percent Similarity: 98.14% Conservative: 0
Best Local Similarity: 98.14% Mismatches: 4
Query Match: 98.31% Indels: 0
DB: 5 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-029-191-1 (1-3108)

Qy 1 MetProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 78 ATGCCTGCCTTCAACAGATTGCTTCCCTAGCTTCTCTAGTGTCTCATCTACTGGGTGAGA 137

Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 138 GTCTGCTTCCCTGTGTGTGGAAGTCCCTCGGAGACAGAGCGGTGCAGGGCAATCCC 197

Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluValGluAlaThrValVal 60
Db 198 ATGAAGCTGAGGTGCATCTCTGCATGAAGAGGAGGAGGTGGAGGCCACCATCTGTGTG 257

Qy 61 GluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 258 GAGTGGTTCTACAGCCCTGAGGCGGTAAAGATTTCTTATATAGTATCGGAATGGC 317

Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 318 CACCAGGAAGTGGAGAGCCCTTCCAGGCGGTCTGCAGTGGAAATGGGAGCAAGACCTG 377

Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 378 CAGGACGTATCCATCACTGCTACTCAATGTCACTTTGAATGACTCTGGCTCTACACATGC 437

Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrArgLeu 140
Db 438 AATGTGTCAGGAGTTCGAATTCGAGGCACACAGGCCCTTTTGTGAAGACCAACGAGACTG 497

Qy 141 IleProLeuArgValThrGluAlaGlyGluAspPheThrSerValSerGluIle 160
Db 498 ATACCTTTGCGAGTCACTGAAGAGCGGAGAAAGACTTCACTCCGTGGTCTCGGAATC 557

Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 558 ATGATGTACATCCTCCTGCTTCTCCTACCTTGTGGCTGTTTATTGAGATGATCTATTGC 617

Qy 181 TyrArgLysValSerLysAlaGluAlaGlnGluAsnAlaSerAspTyrLeuAla 200
Db 618 TACAGAAAGGTCTCTAAGGCCGAGAGGACACAGGAAATGCGTCTGACTACCTTGTCT 677

Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 678 ATCCCTTCAGAGAACAGAGAACTCTGTGGTACCCTGTGGAGGAA 722

RESULT 7
US-10-450-763-22568
```

; Sequence 22568, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIORITY FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22568
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (518)..(1051)
; OTHER INFORMATION: 91% homologous to Homo sapiens voltage-gated sodium channel
; OTHER INFORMATION: beta-3 subunit, accession number AJ243396, Smith-Waterman Score=826
US-10-450-763-22568

Alignment Scores:
Pred. No.: 3,17e-116 Length: 1195
Score: 927.50 Matches: 184
Percent Similarity: 94.42% Conservative: 2
Best Local Similarity: 93.40% Mismatches: 9
Query Match: 82.52% Indels: 2
DB: 9 Gaps: 1

US-09-977-579A-2 (1-215) x US-10-450-763-22568 (1-1195)

Qy	1	MetProLapheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer	20
Db	463	ATGCCTGCCTCAATAGATTGTTTCCCTGGCTTCTCTCGTGTATCTACTAGTCAGT	522
Qy	21	ValCysPheProValCysValGlu-ValProSerGluThrGluAla---ValGlnGlyAs	39
Db	523	GTCTGCTTCCCTGTGTGGGGGGAAGTGCCCTTAGAAAAAGGGGGGGCAGCGGTAA	582
Qy	39	nProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrVa	59
Db	583	CCCCATGAAGTCGCTGCATCTCTTCATGAGAGAGAGAGGTTGGAGGCCACACGGT	642
Qy	59	lValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArgAs	79
Db	643	GGTGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTATTATTCAGATATCGAA	702
Qy	79	nGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAs	99
Db	703	TGGCCACACAGAGGTGGAGAGCCCTTTTCAGGGCGCTTCAGTGGGAATGACAAAGGA	762
Qy	99	pLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrTh	119
Db	763	CCTCAGAGACGTGCTCATCTGTGCTCAAGCTCACTCTGAACGACTCTGGCCCTCTACAC	822
Qy	119	rCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThrAr	139
Db	823	CTGCAATGTGTCCTGGAGTTTGATTTGAGCGCATCGGCCCTTTGTGAAGACGACGCG	882
Qy	139	gLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGl	159
Db	883	GCTGATCCCCCTAAGAGTACCGAGGAGGCTTTCACCTCTGTGGTCTCAGA	942
Qy	159	uIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTy	179
Db	943	AATCATGATGATACATCTTCTGGTCTTCCCTCACCTTGTGGCTGCTCATCGAGATGATATA	1002

Qy	179	rCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGlnGluAsnAla	195
Db	1003	TTGCTACAGACAGGTCTCAAAAGCCGAAGAGGAGGCCCAAGAAACGCG	1051

RESULT 8
US-10-450-763-22567
; Sequence 22567, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIORITY FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 22567
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (300)..(407)
; OTHER INFORMATION: 94% homologous to Homo sapiens putative kruppel-related zinc
; OTHER INFORMATION: finger protein NY-REN-23 antigen, accession number AF155101, Smith-
; OTHER INFORMATION: Waterman Score=180.
US-10-450-763-22567

Alignment Scores:
Pred. No.: 2e-83 Length: 3531
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.74% Indels: 0
DB: 9 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-450-763-22567 (1-3531)

Qy	19	ValSerValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGly	38
Db	2959	GTCAAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCTCGGAGAGGAGGCCGTGACGGGC	3018
Qy	39	AsnProMetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThr	58
Db	3019	AACCCCATGAAGCTGGCTGCATCTCTGCATGAAGAGAGAGAGGTGGAGGCCACCAAG	3078
Qy	59	ValValGluTrpPheTyrArgProGluGlyGlyLysAspPheLeuIleTyrGluTyrArg	78
Db	3079	GTGGTGAATGGTTCTACAGCCCGAGGGCGGTAAAGATTTCCTATTATTCAGATATCGG	3138
Qy	79	AsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLys	98
Db	3139	AATGGCCACACAGAGGTGGAGAGCCCTTTTCAGGGGGCCCTGCAGTGAATGGCAGCAAG	3198
Qy	99	AspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyr	118
Db	3199	GACCTGCAGGACGTGCTCATCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA	3258
Qy	119	ThrCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLysThrThr	138
Db	3259	ACCTGCAATGTGTCGGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGACG	3318
Qy	139	ArgLeuIleProLeuArgValThrGluGlu	148
Db	3319	CGGCTGATCCCTTAAAGATCAACGAGGAG	3348

RESULT 9


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Db 123 ACGACGGCGGTGATCCCCCTTAAGAGTCACCGAGAGGCTGGAGAGGACTTCACCTCTGTG 182
Qy 157 ValSerGluLeuMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGlu 176
Db 183 GTCTCAGAAATCATGATGATACATCTTCTGGTCTTCCTCACCTGTGGCTGCTCATCGAG 242
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSer 196
Db 243 ATGATATATTGCTACAGAAAGTCTCAAAAGCCGGAAGAGGAGCCCAAGAAACCGCTCT 302
Qy 197 AspTyrLeuAlaIleProSerGluAsnLysGluSerAlaValProValGluGlu 215
Db 303 GACTACCTTGCCATCCCATCTGAGAACAGAGAACTCTGCGGTACCAGTGGAGGAA 359

RESULT 12
US-11-060-756-7089
; Sequence 7089, Application US/11060756
; Publication No. US200502213541
; GENERAL INFORMATION:
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7089
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-7089

Alignment Scores:
Pred. No.: 1,98e-71 Length: 600
Score: 598.00 Matches: 119
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 53.20% Indels: 0
DB: 10 Gaps: 0

US-09-977-579A-2 (1-215) x US-11-060-756-7089 (1-600)

Qy 97 SerLysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 3 AGCAAGGACCTGCGAGGCGTGTCTCATCTACTGTCTCAACGTCACTCTGAACGACTCTGGC 62
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArgProPheValLys 136
Db 63 CTCTACACCTGCAATGTGTCCCGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAG 122
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluAlaGlyGluAspPheThrSerVal 156
Db 123 ACGACGGCGGTGATCCCCCTTAAGAGTCACCGAGAGGCTGGAGAGGACTTCACCTCTGTG 182
Qy 157 ValSerGluLeuMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuLeuIleGlu 176
Db 183 GTCTCAGAAATCATGATGATACATCTTCTGGTCTTCCTCACCTGTGGCTGCTCATCGAG 242
Qy 177 MetIleTyrCysTyrArgLysValSerLysAlaGluGluAlaAlaGlnGluAsnAlaSer 196
Db 243 ATGATATATTGCTACAGAAAGTCTCAAAAGCCGGAAGAGGAGCCCAAGAAACCGCTCT 302
Qy 197 AspTyrLeuAlaIleProSerGluAsnLysGluSerAlaValProValGluGlu 215
Db 303 GACTACCTTGCCATCCCATCTGAGAACAGAGAACTCTGCGGTACCAGTGGAGGAA 359

RESULT 13
US-10-029-191-23
; Sequence 23, Application US/10029191
; Publication No. US20020160453A1
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; GENERAL INFORMATION:
; APPLICANT: CURTIS, RORY A.J.
; TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; FILE REFERENCE: 210147.00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/569,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Lepus Sp.
US-10-029-191-23

Alignment Scores:
Pred. No.: 9,49e-55 Length: 657
Score: 477.00 Matches: 106
Percent Similarity: 64.49% Conservative: 32
Best Local Similarity: 49.53% Mismatches: 68
Query Match: 42.44% Indels: 8
DB: 5 Gaps: 5

US-09-977-579A-2 (1-215) x US-10-029-191-23 (1-657)

Qy 10 LeuAlaSerLeuValLeuIleTyrTrpValSerValCysPheProValCysValGluVal 29
Db 13 CTGGCTTTCTGGTGTGGCGCGCGCTGTCTTCGCGCTGGGGGGCTCGGTGGAGGTG 72
Qy 30 ProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMet 49
Db 73 GACTCGAGACCGAGCCGTGTACGGGATGACCTTCANAAATTCTGTGCATCTCTCTGCAAG 132
Qy 50 LysArgGluGluValGluAlaThrThrValValGluTrpPheTyrArgProGluGlyGly 69
Db 133 CGCGCGCAGCAGACACCGCGCGAGACCTTCACGAGTGGACCTTCGCGCAGAAAGGCACT 192
Qy 70 LysAspPheLeu---IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerPro--- 87
Db 193 GAGGAGTTCTGTAAGATCTTCGCGCTATGAGACGAGGTCTGCAGCTGGAGAGACGAG 252
Qy 88 ---PheGlnGlyArgLeuGlnTrpAsnGlySer-----LysAspLeuGlnAspVal 103
Db 253 CGCTTTGAGGCGCGGTGTGTGGACGCGCGCGGACCAAGGACCTTCGAGGACCTG 312
Qy 104 SerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSer 123
Db 313 TCCATCTTCATCACCATGTCACTACACCACTCGCGGCGACTACCAAGTGCCTGTCTAC 372
Qy 124 ArgGluPheGluPheGluAlaHisArgProPheValLysThrArgLeuIleProLeu 143
Db 373 CGCTGCTCTCTCTCGAAAACTACGAGCACACACCGCGCTCGTCAAGAGATCCACCTG 432
Qy 144 ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTyr 163
Db 433 GAGGTGTGGACAAAGGCCAACAGACATGGCATCCATCGTGTGGAGATCATGATGTAC 492
Qy 164 IleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCysTyrArgLys 183
Db 493 GTGCTCATCGTGTGTGTGACCATCTGGCTCGTGGCGAGATGGTGTGTCTCTACCAAG 552
Qy 184 ValSerLysAla---GluGluAlaAlaGlnGluAsnAlaSerAspTyrLeuAlaIlePro 202
Db 553 ATCGCGCGCGCCACCGGAGGCGCGGCGAGAGACGCTTCGGAATACTTTGGCCATCAC 612
Qy 203 SerGluAsnLysGluAsn---SerAlaValProValGluGlu 215
Db 613 TCAGAAAGCAAGAAATAATTCCACGGCGCTCCAGGTGGCTGAA 654
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RESULT 14
US-10-723-860-2247
; Sequence 2247, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziiz, Nataasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 03682.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723.860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2247
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2247

Alignment Scores:
Pred. No.: 1.01e-53 Length: 1335
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: Gaps: 6

US-09-977-579A-2 (1-215) x US-10-723-860-2247 (1-1335)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db GCCATGGGGAGGCTG-----CTGGCCTTAGTGTGGCGCGGCACCTGGTCTCTCAGCC 75

Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db TCGCGGGGCTCGTGGAGGTGACTCGGAGACCGAGCCGCGTATGGATGACCTTCAA 135

Qy 43 LeuArgCysIleSerCysMetLysArgGluValGluAlaThrValValGluTrp 62
Db ATTTCTTTCATCTCTCTGCAAGCGCGCAGCAGACCAACGCTGAGACCTTCAACGAGTGG 195

Qy 63 PheTyrArgProGluGlyGlyAspPheLeu----IleTyrGluTyrArgAsnGlyHis 81
Db ACCTTCCGCCAGAGGGCACTGAGGAGTTTGTCAAGATCCTCGCGCTATGAGAATGAGGTG 255

Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db TTGCAGCTGGAGGAGGATGAGCGCTTCAGGGCCGCGTGGTGGATGGCAGCGCGGGC 315

Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db ACCAAGACCTGCAGGATCTGTCTATCTCATCCCATGTGTCACCAACCACTCGGGC 375

Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db GACTACGAGTGCACGCTACCGCTCTCTTCTCGAAACCTACGAGCAACACACGAGC 435

Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db GTCGTCAAGAGATCCACATGAGGTAGTGACCAAGCCCAACAGAGATCGGCATCCATC 495

Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGlu 176
Db GTGCTGAGATCATGATGATGTCTCATTTGTGGTGTGACCATATGCTCGTGGCAGAG 555

Qy 177 MetIleTyrCysTyrArgLysValSerLysAla----GluGluAlaAlaGlnGluAsnAla 195
Db ATGATTTACTGTACAAGAAGATCGTCGCCGCCAGGAGACTGCTGTCGACGAGGAATGCC 615

Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
Db TCGGAATACCTGGCCATCACTCTGAAAGCAAGAGAACTGCACGGCGCTCCAGGTGGCC 675

Qy 215 Glu 215
Db GAA 678

RESULT 15
US-10-477-272-1
; Sequence 1, Application US/10477272
; Publication No. US20040191791A1
; GENERAL INFORMATION:
; APPLICANT: Biomimetics Limited
; TITLE OF INVENTION: P12
; FILE REFERENCE: SCN1B (R85C)
; CURRENT APPLICATION NUMBER: US/10/477,272
; CURRENT FILING DATE: 2003-11-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1414
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-477-272-1

Alignment Scores:
Pred. No.: 1.1e-53 Length: 1414
Score: 473.00 Matches: 109
Percent Similarity: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: Gaps: 6

US-09-977-579A-2 (1-215) x US-10-477-272-1 (1-1414)

Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db GCCATGGGGAGGCTG-----CTGGCCTTAGTGTGGCGCGGCACCTGGTCTCTCAGCC 151

Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db TCGCGGGGCTCGTGGAGGTGACTCGGAGACCGAGCCGCGTATGGATGACCTTCAA 211

Qy 43 LeuArgCysIleSerCysMetLysArgGluValGluAlaThrValValGluTrp 62
Db ATTTCTTTCATCTCTCTGCAAGCGCGCAGCAGACCAACGCTGAGACCTTCAACGAGTGG 271

Qy 63 PheTyrArgProGluGlyGlyAspPheLeu----IleTyrGluTyrArgAsnGlyHis 81
Db ACCTTCCGCCAGAGGGCACTGAGGAGTTTGTCAAGATCCTCGCGCTATGAGAATGAGGTG 331

Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db TTGCAGCTGGAGGAGGATGAGTGTCTCGAGGGCCGCGTGGTGGATGGCAGCGGGC 391

Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db ACCAAGACCTGCAGGATCTGTCTATCTCATCCCATGTGTCACCAACCACTCGGGC 451

Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db GACTACGAGTGCACGCTACCGCTCTCTTCTCGAAACCTACGAGCAACACACGAGC 511

Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db GTCGTCAAGAGATCCACATGAGGTAGTGACCAAGCCCAACAGAGATCGGCATCCATC 571

Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGlu 176
Db GTGCTGAGATCATGATGATGTCTCATTTGTGGTGTGACCATATGCTCGTGGCAGAG 631

Qy 177 MetIleTyrCysTyrArgLysValSerLysAla----GluGluAlaAlaGlnGluAsnAla 195

				:: :::						691
Db	632	ATGATTACTGCTACAAAGAAATCGCTCCGCCACGGAGACTGTGCACAGAGAATGCC								
Qy	196	SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu								214
							---	---	---	
Db	692	TCCGAATACCTGGCCATCACCTCTGAAGCAAGAGAACTGCACGGCGCTCCAGGTGCC								751
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Db	752	GAA	754							

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GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: December 13, 2005, 17:21:42 ; Search time 179 Seconds
(without alignments)
449.043 Million cell updates/sec

Title: US-09-977-579A-2

Perfect score: 1124

Sequence: 1 MPANRLPLASLVLVWVS.....SDYLAIPTSENKENSAPVVEE 215

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
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Database :

Published Applications NA New:
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2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1124	100.0	1261	US-10-374-954-8
2	473	42.1	1335	US-10-374-954-4
3	241	21.4	880	US-10-750-185-44336
4	165.5	14.7	150468	US-11-112-908-56
5	165.5	14.7	193789	US-11-112-908-55
6	147	13.1	673	US-11-080-991-111
7	147	13.1	1371	US-10-131-826A-487
8	131	11.7	1777	US-10-131-826A-529

Alignment Scores: 5.8e-139 Length: 1261
Pred. No.: 1124.00 Matches: 215
Score: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

ALIGNMENTS

RESULT 1
US-10-374-954-8
; Sequence 8, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10374,954
; PRIOR FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 1261
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (376)..(1023)
US-10-374-954-8

Sequence 6, Appli
Sequence 519, App
Sequence 387, App
Sequence 44339, A
Sequence 80, Appl
Sequence 44343, A
Sequence 62, Appl
Sequence 367, App
Sequence 385, App
Sequence 49, Appl
Sequence 30397, A
Sequence 367, App
Sequence 13, Appl
Sequence 31, Appl
Sequence 77, Appl
Sequence 8, Appli
Sequence 7, Appli
Sequence 48, Appl
Sequence 516, App
Sequence 60713, A
Sequence 27, Appl
Sequence 44, Appl
Sequence 6, Appli
Sequence 83, Appli
Sequence 1, Appli
Sequence 39, Appl
Sequence 37, Appl
Sequence 156, App
Sequence 158, App
Sequence 7, Appli
Sequence 94, Appl
Sequence 45, Appl
Sequence 95, Appl
Sequence 242, App
Sequence 36, Appl
Sequence 96, Appl
Sequence 42, App

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DB: 6 Gaps: 0
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Qy 1 MetProLaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSer 20
Db 376 ATGCTGCTCCTCAATAGATTGTTTCCCTGCTGCTCTCTCGTGTATCTACTAGGGTCAGT 435
Qy 21 ValCysPheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnPro 40
Db 436 GTCTGCTTCCCTGTGTGTGAAGTGCCTTCGAGACGGAGCGCTGCAGGGCAACCC 495
Qy 41 MetLysLeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrValVal 60
Db 496 ATGAAGCTGCCTGCATCTCTGTCATGAGAGAGAGAGGGTGGAGCCACACCGTGGTG 555
Qy 61 GluTrpPheTyrArgProGluGlyCysLysAspPheLeuIleTyrGluTyrArgAsnGly 80
Db 556 GAATGGTTCTACAGCCCGAGGGCGGTAAGATTTCCTTATTTACGAGTATCGGAATGGC 615
Qy 81 HisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 616 CACCAGGAGGTGGAGAGCCCTTTTCAGGGGCGCTCGAGTGGAAATGGCAGGACCTG 675
Qy 101 GlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 676 CAGGAGGTGTCATCACTGCTCACTGCTCACTCTGACGACTCTGGCTCTACACCTGC 735
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 736 AATGTGTCCTGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGTG 795
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGluIle 160
Db 796 ATCCCTTAAGATCACCAGGAGGCTGGAGAGGACTTCACTCTGTGTGCTCAGAAATC 855
Qy 161 MetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyrCys 180
Db 856 ATGATGATACATCTTCTGCTCTCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
Qy 181 TyrArgLysValSerLysAlaGluGluAlaGlnGluAlaGlnGluAlaSerAspTyrLeuAla 200
Db 916 TACGAAAGGCTCAAAAGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 975
Qy 201 IleProSerGluAsnLysGluAsnSerAlaValProValGluGlu 215
Db 976 ATCCCATCTGAGAACAGGAGAACTCTCGGTACCAGTGGAGAA 1020
RESULT 2
US-10-374-954-4
; Sequence 4, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L.
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; TITLE OF INVENTION: BRAIN VOLTAGE-GATED SODIUM CHANNEL, SCN1A
; FILE REFERENCE: 1242/41/2
; CURRENT FILING DATE: US/10/374,954
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/359,382
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(681)
US-10-374-954-4
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Alignment Scores: 2,79e-52 Length: 1335
Pred. No.: 473.00 Matches: 109
Score: 63.35% Conservative: 31
Best Local Similarity: 49.32% Mismatches: 71
Query Match: 42.08% Indels: 10
DB: 6 Gaps: 6
US-09-977-579A-2 (1-215) x US-10-374-954-4 (1-1335)
Qy 3 AlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerValCys 22
Db 22 GCCATGGGGAGGGCTG-----CTGGCCTTAGTGTGGCGCGGACTGGTGTCTCTCAGCC 75
Qy 23 PheProValCysValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLys 42
Db 76 TGGGGGGGGCTGCGTGGAGGTGGACTCGAGACCGAGGCGGTATGGATGACCTTCAAA 135
Qy 43 LeuArgCysIleSerCysMetLysArgGluGluValGluAlaThrThrValValGluTrp 62
Db 136 ATTCTTTGCACTCTCTGCAAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 195
Qy 63 PheTyrArgProGluGlyGlyLysAspPheLeu---IleTyrGluTyrArgAsnGlyHis 81
Db 196 ACCTTCGCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 255
Qy 82 GlnGluValGluSerPro-----PheGlnGlyArgLeuGlnTrpAsnGlySer----- 97
Db 256 TTGCAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 315
Qy 98 ---LysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAspSerGly 116
Db 316 ACCAAGAGCTTGAGGATCTGCTATCTTCACTCACTCACTCACTCACTCACTCACTCGGC 375
Qy 117 LeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPheValLys 136
Db 376 GACTACGAGTGCCACGCTACCGCTCTCTTTCGAAAGTACGAGGAGCAACACGAGC 435
Qy 137 ThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerVal 156
Db 436 GTCGTCAAGAGATCCCATTTGAGGTAGTGACAAAGCCCAACAGAGACATGGCATCCATC 495
Qy 157 ValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeuIleGlu 176
Db 496 GTGCTCGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 555
Qy 177 MetIleTyrCysTyrArgLysValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db 556 ATGATTTACTCTACAAGAGATCGCTGCCCGCAGGAGACTGCTGCACAGGAGAAATGCC 615
Qy 196 SerAspTyrLeuAlaIleProSerGluAsnLysGluAsn---SerAlaValProValGlu 214
Db 616 TCGGAATACCTGGCCATCACCTCTCTGAAAGCAAGAGAACTGCACGGGCGTCCAGGTGGCC 675
Qy 215 Glu 215
Db 676 GAA 678
RESULT 3
US-10-750-185-44336
; Sequence 44336, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
```


Db 108996 GAAGAGGATATTCAATTTTACAATTGAAGAAACAGAGG-----CCTAGAGACATTTGAGTC 109049
Qy 86 rProPheGlnGlyArgLeu-----GlnTrp-----AsnGlySerLysAs 99
Db 109050 ACTTCGCAAGGTCAACACAGCTGGCCAGTGGCAGAGCCAGCGCTTTGAACCTGAGCCTTCT 109109
Qy 99 pLeuGlnAspValSerIle-----ThrValLeuAsnValThrLeuAsnAspSerGlyLe 117
Db 109110 GGTTCAGAGCTACGGCTTTTAGGCACCGTCTGAGGGCCCTCCAG-AATGACACAGATGT 109168
Qy 117 uTyThrCysAsnValSerArgGluPheGluPheGluAlaHisArg----- 132
Db 109169 GGCCTCGAGTTACACAGGGGAGCAGTTGAGGGTGACCCCAAGGCT 109228
Qy 133 -----ProPheValLysThrThrArgLeuProLeu----- 143
Db 109229 GGGTATTAAATCAAGTGCATACACAGGCCAGGGAGGTGAGCCATCTCCAAGC 109288
Qy 143 ----- 143
Db 109289 TCACAGCAAGCTCACAGCACTCAGGCTGTCTATGCAGCGCTGGGCTACCCCTTAACC 109348
Qy 144 -ArgValThrGluGluAlaGlyGluAspPheThrSerValValSerGluIleMetMetTy 163
Db 109349 CTGCTGGCCCTGCAGGCCAACAGAGACATGGCATCCATCGTGTCTGAGATCATGATGA 109408
Qy 163 rIleLeuLeuValPheLeuThrLeuTrpLeuIleGluMetIleTyCysTyArgLy 183
Db 109409 TGTGCTCATTTGGTGTGACCATATGCTCGTGGCAGAGATGATTTACTGCTACAAGAA 109468
Qy 183 sValSerLysAla---GluGluAlaAlaGlnGluAsnAla 195
Db 109469 GATCGCTGCCGCCAGGAGACTGCTGCACAGGAGATGCG 109508

RESULT 6

US-11-080-991-111
; Sequence 111, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-080-991-111

Alignment Scores:

Pred. No.: 2.38e-09 Length: 673
Score: 147.00 Matches: 57
Percent Similarity: 41.44% Conservative: 35
Best Local Similarity: 25.68% Mismatches: 80
Query Match: 13.08% Indels: 50
Dbs: 7 Gaps: 9

US-09-977-579A-2 (1-215) x US-11-080-991-111 (1-673)

Qy 7 LeuPheProLeuAlaSerLeuValLeuIleTyTrpValSerValCysPheProValCys 26
Db 89 CTTTGGCCTATAGCAGCT---GTGAAATTTATACCTCCGGTG----- 130
Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 131 -----CTGAGGCTGTTAATGGACAGATGCTCGGTAAATGCAC 172

Qy 47 SerCysMetLysArgGluGluValGluAlaThrThrValValGluTrpPheTyArgPro 66
Db 173 TTCTCCAGCTTGGCCCTGTGGGTGATGCTCTAACAGTGACC---TGAATTTTCGTCT 229
Qy 67 ---GluGlyGly---LysAspPheLeuIleTyTrpGluTyArgAsnGlyHisGlnGluVal 84
Db 230 CTAGACGGGGACCTGAGCAGTTTGTATTCTTACTTACCACATAGATCCCTTCCAAACCCATG 289
Qy 85 GluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSer 104
Db 290 AGTGGCGGTTTAAGGACCGGGTCTTGGGATGGGAATCCTGAGCGGTACGATGCTCTCC 349
Qy 105 IleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyTrpCysAsnValSerArg 124
Db 350 ATCCTTCTCTGGAACCTGCAGTTCGACGACAAATGGGACATACACTGCCAGGTGAAGAAC 409
Qy 125 GluPheGluPheGluAlaHisArgProPheValLysThrThrArgLeuIleProLeuArg 144
Db 410 -----CCACTGAT 418
Qy 145 ValThrGluGluAlaGlyGluAspPheThrSerValVal-----SerGlu 159
Db 419 GTTGATGGGTGATAGGGAGATCCGGCTCAGCGTCTGCACACTGTACGCTTCTCTGAG 478
Qy 160 IleMetMetTyTrpIleLeuLeuVal-----PheLeuThrLeuTrpLeu 173
Db 479 ATCAGCTCTCGGCTCTGGCCATTTGGCTCTGCTGTCGACTGATGATCAATAAGTAATT 538
Qy 174 LeuIleGluMetIleTyCysTyArgLysValSerLysAlaGluGluAlaGlnGlu 193
Db 539 GTAGTGTCTCTCTCCAGCATTTACCGGAAAAAGCGATGGGCGGAAAGAGCT----- 589
Qy 194 AsnAlaSerAspTyTrpLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 590 -----CATAAAGTGGTGAGATAAAATCAAAAGAGAGAGAAAGCTCAACCAA 637
Qy 214 GluGlu 215
Db 638 GAGAAA 643

RESULT 7

US-10-131-826A-487
; Sequence 487, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113


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Qy 27 ValGluValProSerGluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIle 46
Db 280 GTATATACCCCAAGAAATCTTGGTGCMAATGGTACACAAAGGGAAGCTGACCTGC--- 336
Qy 47 SerCysMetLysArgGluGluValGluAlaThr-----ThrValValGluTrpPhe 63
Db 337 -----AAGTTCAAAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTCTCTGTGAGC 387
Qy 64 TyrArgProGluGlyGlyLysAspPheLeu---lleTyrGluTyrArgAsnGlyHisGln 82
Db 388 TTCAGCCAGAGGGGGCGGACACTACTGTGTGCTGTTTCCACTACTCCCAAGGCAAGTG 447
Qy 83 GluValGluSer-----ProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeu 100
Db 448 TACCTTGGGAATTATCCACCACTTTAAAGACAGAATCAGCTGGCTGGAGACCTTGCACAAG 507
Qy 101 GlnAspValSerlleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys 120
Db 508 AAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT 567
Qy 121 AsnValSerArgGluPheGluAlaHisArgProPheValLysThrThrArgLeu 140
Db 568 GATGTCAAAAC----- 579
Qy 141 IleProLeuArgValThrGluGluAlaGlyGluAspPheThrSerValSerGlu--- 159
Db 580 ---CCTCTGCATCGTTGTCAGCTGCAGCCGACACATAGGCTCTATGTCGTAGAAAAAGAG 636
Qy 160 -----lleMetMetTyrIleLeuLeuValPheLeuThr 170
Db 637 AATTGGCTGTGTTTCCAGTTTGGGTAGTGGTGGCATAGTTACTGTGTGGTCTTAGGT 696
Qy 171 LeuTrpLeuIleGluMetIleTyrCys-----TyrArgLys----- 183
Db 697 CTCACTGTCTCATCAGCATGATTCTGGCTGTCTCTATAGAGAAAAAACTCTAAACGG 756
Qy 184 -----ValSerLysAlaGluGluAlaAlaGlnGlu 193
Db 757 GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCCACAGTTAAGCAGGCTCTCGGAAG 816
Qy 194 AsnAlaSerAsp-----TyrLeuAlaIleProSerGluAsnLysGluAsnSer 209
Db 817 TCCCTCCGACACTGAGGGTCTTTGTAAGAGTCTGCTTCTGATCTCACCAGGGGCCA 876
Qy 210 AlaVal 211
Db 877 GTCATA 882

RESULT 9
US-10-374-954-6
; Sequence 6, Application US/10374954
; Publication No. US20050260576A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: George, Alfred L
; APPLICANT: Lossin, Christoph
; TITLE OF INVENTION: HETEROLOGOUS EXPRESSION SYSTEM FOR STUDYING RECOMBINANT HUMAN
; FILE REFERENCE: 1242/41/2
; CURRENT APPLICATION NUMBER: US/10/374,954
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: US 60/359,382
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 6
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(648)
US-10-374-954-6
```

```
Alignment Scores:
Pred. No.: 0.000162 Length: 648
Score: 110.50 Matches: 55
Percent Similarity: 45.33% Conservative: 42
Best Local Similarity: 25.70% Mismatches: 88
Query Match: 9.83% Indels: 29
DB: 6 Gaps: 11

US-09-977-579A-2 (1-215) x US-10-374-954-6 (1-648)

Qy 2 ProAlaPheAsnArgLeuPheProLeuAlaSerLeuValLeuIleTyrTrpValSerVal 21
Db 28 CTGCGCTTCAGC-----CTCAGCGGGCTCAGTCTCTTTTC-----TCATTG 69
Qy 22 CysPhePro-----ValCysValGluValProSerGluThrGluAlaValGlnGly 38
Db 70 GTGCCACAGAGCGGACATGGAGGTACAGTACTCTGCCACCTCCCAAGTCTCAATGGC 129
Qy 39 AsnProMetLysLeuArgCysIle-----SerCysMetLysArgGluGluValGluAla 56
Db 130 TCTGACGCGCTGCGCTGCACCTTCAACTCTCTGTACACAGTGAACCAACAGATTC 189
Qy 57 ThrThrValValGluTrpPheTyrArgProGluGlyGly-----LysAspPheIleu 73
Db 190 TCC-----CTGAACCTGGACTTACCAGGAGTGCACAACTGCTCTGAGGAGATGTTCTC 243
Qy 74 IleTyrGluTyrArgAsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGln 93
Db 244 CAGTTCGCGATGAAGATCATTAACCTGAAGCTGAGCGG---TTTCAAGCCGCGTGGAG 300
Qy 94 TrpAsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsn 113
Db 301 TTCTCAGGAAACCCCAAGTAGTGTGCGGTGATGCTGAGAAACGTGCAGCCGAG 360
Qy 114 AspSerGlyLeuTyrThrCysAsnValSerArgGluPheGluPheGluAlaHisArgPro 133
Db 361 GATGAGGGGATTTACAACTGCTACATCATGAAC-----CCCCCTGACCGCACCGTGGC 414
Qy 134 PheValLysThrThrArgLeuIleProLeuArgValThrGluGluAlaGlyGluAspPhe 153
Db 415 CATGGCAAG-----ATCCATCTGAGGTCTCTATGGAAGACCCCTGAGCGG 462
Qy 154 ThrSerValValSerGluIleMetMetTyrIleLeuLeuValPheLeuThrLeuTrpLeu 173
Db 463 GACTCCACGGTGGCGGTGATTGTGGGTGCTCGCGGGGCTTCTTGGCTGTGCTCATC 522
Qy 174 LeuIleGluMetIleTyr-----CysTyrArgLysValSerLysAlaGluGluAlaGln 192
Db 523 TTGGTGTGATGTTGTTGTTCAAGTGTGTGAGGAGA-----AAAAAAGAGCAG 567

Qy 193 GluAsnAlaSerAspTyrLeuAlaIleProSerGluAsnLys 206
Db 568 AAGCTGACACAGATGACCTGAAGACCGGAGGAGGGGCAAG 609
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RESULT 10
US-10-131-826A-519
; Sequence 519, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
```



```
Best Local Similarity: 24.88% Mismatches: 69
Query Match: 9.65% Indels: 55
DB: 6 Gaps: 10

US-09-977-579A-2 (1-215) x US-10-131-826A-387 (1-2458)
Qy 18 TrpValSerValCysPheProValCysValGluValProSer----- 31
Db 550 TGGAGCCATGTCATCTTAAAGTCTTAGTGAGA---CCATCCAAAGCCCAAGTGTGAGTTG 606
Qy 32 GluThrGluAlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMetLysArg 51
Db 607 GAAGAGAGCTGACAGAGGAAGTACCTGACTTTGCAGTGTGAGTATCATCTCTCGGCACA 666
Qy 52 GluGluValGluAlaThrThrValValGluTrp---PheTyrArgProGluGlyGlyLys 70
Db 667 GAGCCCAT-----GTATTACTGGCAGCGAATCCGAGAGAAAGAGGGAGAG 714
Qy 71 AspPheLeuIleTyrGluTyrArgAsnGlyHisGlnGluValGluSerProPheGlnGly 90
Db 715 GATGACGCTCG-----CCTCCCAATCT 738
Qy 91 ArgLeuGlnTrpAsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnVal 110
Db 739 AGGATTGACTACAAC-----CACCCCTGGACGAGTTCTGCTGCAGAACTTT 783
Qy 111 ThrLeuAsnAspSerGlyLeuTyrThrCysAsnValSerArgGluPheGluAla 130
Db 784 ACCATGTCTCTACTCTGGACTGTACAGTGCACAGCAGCAACGAGCTGGGAAGGAAGC 843
Qy 131 HisArgProPheValLysThrArgLeuIleProLeuArgValThrGluAlaGly 150
Db 844 -----TGTGTGGTGCAGTAACGTACAGTATGTA 873
Qy 151 GluAspPheThrSerVal-----ValSerGluIleMetMetTyrIleLeuVal 167
Db 874 CAAAGCATCGCGTGTGTCAGGAGCAGTGCACAGCAGTGTGGTGGAGCCCTGCTGATT 933
Qy 168 PheLeuThrLeuTrpLeuLeuGluMetIleTyrCysTyrArgLysValSerLysAla 187
Db 934 TTCCTCTTGGTGGCTGCTAATC-----CGAAGGAAGAACAAAGAA 975
Qy 188 GluGluAlaAlaGlnAsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGlu 207
Db 976 AGATATGAGGAAGAGAGAGA-----CCTAATGAATTCGAGAA 1014
Qy 208 AsnSerAlaValPro 212
Db 1015 GATGCTGAAGCTCCA 1029

RESULT 12
US-10-750-185-44339
; Sequence 44339, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922-31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44339
; LENGTH: 1497
; TYPE: DNA

; ORGANISM: Bovine 19866880940727
US-10-750-185-44339
Alignment Scores:
Pred. No.: 0.00318 Length: 1497
Score: 105.00 Matches: 21
Percent Similarity: 95.45% Conservative: 0
Best Local Similarity: 95.45% Mismatches: 1
Query Match: 9.34% Indels: 0
DB: 6 Gaps: 0

US-09-977-579A-2 (1-215) x US-10-750-185-44339 (1-1497)
Qy 194 AsnAlaSerAspTyrLeuAlaIleProSerGluAsnLysGluAsnSerAlaValProVal 213
Db 1289 AACAGGTCCTGACTACCTGGCCATCCATCGAGACAAAGAGAACTCTGCAGTCCAGTG 1348
Qy 214 GluGlu 215
Db 1349 GAGGAA 1354

RESULT 13
US-11-121-086-80
; Sequence 80, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80
; LENGTH: 138821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-80
Alignment Scores:
Pred. No.: 7.33 Length: 138821
Score: 102.50 Matches: 31
Percent Similarity: 40.00% Conservative: 25
Best Local Similarity: 22.14% Mismatches: 63
Query Match: 9.12% Indels: 21
DB: 7 Gaps: 4

US-09-977-579A-2 (1-215) x US-11-121-086-80 (1-138821)
Qy 15 LeuIleTyrTrpValSerValCysPheProValCysValGluValProSerGluThrGlu 34
Db 47246 CTCCTTTTCACAGTATCCAGCATGGCTCAGAAGGTAACCTCAAGCGCAGACTGAAATTTCT 47305
Qy 35 AlaValGlnGlyAsnProMetLysLeuArgCysIleSerCysMetLysArgGluVal 54
Db 47306 GTGGTGGAGAGGAGGATGTGACCTTGGACTGTGTG-----TATGAAACCCGT 47353
Qy 55 GluAlaThrThrValValGluTrpPheTyrArgProGluGlyLysAspPheLeuIle 74
Db 47354 GATACTACTTATTACTTCTGTGTACAGCAACCAACCAAGTGGAGAA-----TTGTTT 47407
Qy 75 TyrGluTyrArgAsnGlyHisGlnGluValGluSerProPheGlnGlyArgLeuGlnTrp 94
Db 47408 TTCCTTATTTCGTCGGAACCTCTTTTGTATGAGCAAAATGAAATGAGTGGTCTTCTTGG 47467
Qy 95 AsnGlySerLysAspLeuGlnAspValSerIleThrValLeuAsnValThrLeuAsnAsp 114
Db 47468 AACTTCCGAAATCCACCAGTTCCTTCACTTCCATCACAGCTCACAGTCTGAGAC 47527
Qy 115 SerGlyLeuTyrThrCysAsnValSerArgGluPheGluAlaHisArgProPhe 134
```


D6	139	ATCTCCTCCAGGCTAGTCTCAGAGCAATTGTACATAGTAATATGGAACACACCTATTTTGCAATGG	198
QY	63	Phe---TyrArgProGluGlycylLysAspPheLeuIleTyrGluTyrArgAsnGlyHis	81
D6	199	TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATAAGTTTCTTAATCGGCTT	258
QY	82	GlnGluValGluSerProPheGlnGlyArgLeuGlnTrpAsnGlySerLysAspLeuGln	101
D6	259	TATGGGGTCCCTGCAGGTTCT-----AGTGGCAGTGGATCAGGCACA	300
QY	102	AspValSerIleThrValLeuAsnValThrLeuAsnAspSerGlyLeuTyrThrCys	120
D6	301	CAITTTTACACTCAAAATCAGACAGATGGAGGCTGAGGATGTTGGGGGTTATTACTGC	357

Search completed: December 13, 2005, 19:15:46
Job time : 327 secs